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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:44:17 ; Search time 47 Seconds
(without alignments)
17.591 Million cell updates/sec

Title: US-10-734-049B-188
Perfect score: 56
Sequence: 1 LMALPPCHAL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	56	100.0	312	2	US-09-230-637-34
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3	56	100.0	313	2	US-09-367-007C-39
4	56	100.0	339	2	US-09-949-016-10160
5	52	92.9	289	2	US-09-252-991A-31795
6	51	91.1	337	2	US-08-757-669A-1
7	51	91.1	337	2	US-09-230-637-22
8	51	91.1	337	2	US-09-230-371A-1
9	48	85.7	290	2	US-09-230-637-32
10	48	85.7	301	2	US-09-230-637-33
11	47	83.9	612	2	US-09-203-895-3
12	46	82.1	322	2	US-09-134-001C-3194
13	46	82.1	324	2	US-09-107-532A-6145
14	46	82.1	325	2	US-09-134-000C-4346
15	44	78.6	44	2	US-09-083-541-3
16	44	78.6	184	2	US-08-907-800A-2
17	44	78.6	184	2	US-08-969-317-2
18	44	78.6	282	2	US-09-540-236-2576
19	44	78.6	286	2	US-09-328-352-8060
20	44	78.6	289	2	US-09-248-796A-18109
21	44	78.6	294	2	US-09-230-637-31
22	43	76.8	161	2	US-09-902-540-14293
23	40	71.4	118	2	US-09-489-039A-14294
24	40	71.4	266	2	US-09-489-039A-10055
25	39	69.6	351	2	US-09-614-912-8
26	37	66.1	1720	1	US-08-477-451-12
27	36	64.3	102	2	US-09-959-392-20

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271	31	55.4	367	2	US-08-832-871B-2	Sequence 2, Appli	344	31	55.4	2787	2	US-09-358-055B-15	Sequence 15, Appl
272	31	55.4	367	2	US-09-476-919-2	Sequence 2, Appli	345	31	55.4	2787	2	US-09-893-238-15	Sequence 15, Appl
273	31	55.4	367	2	US-08-780-311A-2	Sequence 2, Appli	346	31	55.4	5405	2	US-08-718-388-9	Sequence 9, Appli
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335	30	53.6	208	2	US-08-718-904-8	Sequence 8, Appli	468	30	53.6	1053	2	US-09-513-505-6	Sequence 6, Appli
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337	30	53.6	224	2	US-10-104-047-2601	Sequence 2601, Ap	470	30	53.6	1113	2	US-09-252-991A-29215	Sequence 29215, A
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401	30	53.6	249	2	US-09-902-540-14988	Sequence 14988, A	474	29	51.8	19	2	US-09-674-973A-174	Sequence 174, App
402	30	53.6	252	2	US-09-252-991A-18057	Sequence 18057, A	475	29	51.8	22	1	US-08-140-797-12	Sequence 12, Appl
403	30	53.6	259	2	US-09-252-991A-23293	Sequence 23293, A	476	29	51.8	22	1	US-08-486-670A-12	Sequence 12, Appl
404	30	53.6	269	2	US-09-270-767-45987	Sequence 45987, A	477	29	51.8	30	2	US-09-205-258-751	Sequence 751, App
405	30	53.6	270	2	US-09-203-258-568	Sequence 568, App	478	29	51.8	30	2	US-10-004-860-751	Sequence 751, App
406	30	53.6	270	2	US-10-004-860-568	Sequence 568, App	479	29	51.8	41	2	US-09-453-795B-344	Sequence 344, App
407	30	53.6	278	2	US-09-602-777A-76	Sequence 76, Appl	480	29	51.8	42	2	US-09-270-767-62352	Sequence 62352, A
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409	30	53.6	288	2	US-09-270-767-42632	Sequence 42632, A	482	29	51.8	58	2	US-09-461-325-166	Sequence 166, App
410	30	53.6	295	2	US-08-937-067-2	Sequence 2, Appli	483	29	51.8	58	2	US-10-012-542-166	Sequence 166, App
411	30	53.6	295	2	US-09-148-545-179	Sequence 179, App	484	29	51.8	58	2	US-10-115-123-166	Sequence 166, App
412	30	53.6	295	2	US-09-621-011-179	Sequence 179, App	485	29	51.8	63	2	US-08-469-260A-431	Sequence 431, App
413	30	53.6	295	2	US-09-999-833A-415	Sequence 415, App	486	29	51.8	63	2	US-08-488-446-431	Sequence 431, App
414	30	53.6	295	2	US-10-020-445A-415	Sequence 415, App	487	29	51.8	63	2	US-08-467-344A-431	Sequence 431, App
415	30	53.6	296	2	US-09-148-545-237	Sequence 237, App	488	29	51.8	63	2	US-09-621-976-5822	Sequence 5822, Ap
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428	30	53.6	380	2	US-10-104-047-3651	Sequence 3651, Ap	501	29	51.8	86	2	US-10-004-860-750	Sequence 750, App
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451	30	53.6	680	2	US-10-219-541-1	Sequence 1, Appli	524	29	51.8	122	2	US-10-115-123-355	Sequence 355, App
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459	30	53.6	701	2	US-09-949-016-6026	Sequence 6026, Ap	532	29	51.8	136	2	US-10-104-047-3447	Sequence 3447, Ap
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543	29	51.8	163	2	US-09-270-767-31738	Sequence 31738, A	616	29	51.8	375	4	US-09-430-775-28	Sequence 28, Appl
544	29	51.8	163	2	US-09-270-767-46955	Sequence 46955, A	617	29	51.8	375	4	PCT-US94-14436-28	Sequence 28, Appl
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546	29	51.8	178	2	US-09-489-039A-110475	Sequence 10475, A	619	29	51.8	384	1	US-08-673-388-11	Sequence 11, Appl
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551	29	51.8	197	2	US-09-328-352-7839	Sequence 7839, Ap	624	29	51.8	398	2	US-09-489-039A-13756	Sequence 13756, A
552	29	51.8	200	2	US-09-710-279-394	Sequence 394, App	625	29	51.8	401	2	US-08-517-802-3	Sequence 3, Appli
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589	29	51.8	287	2	US-09-501-097A-25	Sequence 25, Appl	662	29	51.8	557	2	US-09-271-815-2	Sequence 14087, A
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591	29	51.8	311	2	US-09-543-681A-5603	Sequence 5603, Ap	664	29	51.8	567	2	US-08-937-067-9	Sequence 9, Appli
592	29	51.8	314	2	US-09-270-767-41822	Sequence 41822, A	665	29	51.8	585	2	US-08-756-317-5	Sequence 5, Appli
593	29	51.8	315	2	US-09-270-767-46735	Sequence 46735, A	666	29	51.8	589	1	US-09-902-540-14944	Sequence 14944, A
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602	29	51.8	350	2	US-09-430-775-32	Sequence 32, Appl	675	29	51.8	681	2	US-08-937-067-14	Sequence 14, Appl
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607	29	51.8	369	1	US-08-052-205-4	Sequence 4, Appli	680	29	51.8	732	2	US-09-198-452A-819	Sequence 819, App
608	29	51.8	369	1	US-08-595-974-4	Sequence 4, Appli	681	29	51.8	837	2	US-09-122-126B-2	Sequence 2, Appli
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688	29	51.8	837	2	US-10-006-768A-317	Sequence 317, App	761	28.5	50.9	570	2	US-09-949-016-9928	Sequence 9928, Ap
689	29	51.8	837	2	US-10-015-671A-317	Sequence 317, App	762	28.5	50.9	570	2	US-09-949-016-9929	Sequence 9929, Ap
690	29	51.8	837	2	US-10-015-333A-317	Sequence 317, App	763	28.5	50.9	570	2	US-09-949-016-9930	Sequence 9930, Ap
691	29	51.8	837	2	US-10-011-833A-317	Sequence 317, App	764	28.5	50.9	570	2	US-09-949-016-9931	Sequence 9931, Ap
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702	29	51.8	1100	2	US-09-949-016-7524	Sequence 7524, Ap	775	28	50.0	12	2	US-09-224-785-15	Sequence 15, Appl
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705	29	51.8	1146	2	US-09-949-016-7567	Sequence 7567, Ap	778	28	50.0	12	2	US-09-756-594-18	Sequence 18, Appl
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707	29	51.8	1270	2	US-09-538-092-1321	Sequence 1321, Ap	780	28	50.0	16	2	US-09-037-742B-11	Sequence 11, Appl
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711	29	51.8	1422	2	US-08-488-446-81	Sequence 81, Appl	784	28	50.0	31	1	US-08-190-802A-159	Sequence 159, App
712	29	51.8	1422	2	US-08-467-344A-81	Sequence 81, Appl	785	28	50.0	31	2	US-08-477-346-159	Sequence 159, App
713	29	51.8	1422	2	US-08-424-550B-81	Sequence 81, Appl	786	28	50.0	31	2	US-08-473-089-159	Sequence 159, App
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715	29	51.8	1798	2	US-09-845-583A-8	Sequence 8, Appli	788	28	50.0	32	1	US-08-452-075-2	Sequence 2, Appli
716	29	51.8	1798	2	US-09-561-709B-11	Sequence 11, Appl	789	28	50.0	32	1	US-09-011-762-6	Sequence 6, Appli
717	29	51.8	1798	2	US-09-917-254-87	Sequence 87, Appl	790	28	50.0	32	2	US-08-851-843A-218	Sequence 218, App
718	29	51.8	1799	2	US-09-845-583A-6	Sequence 6, Appli	791	28	50.0	38	2	US-08-974-549A-337	Sequence 337, App
719	29	51.8	1854	2	US-09-949-016-11625	Sequence 11625, A	792	28	50.0	38	2	US-08-854-050-218	Sequence 218, App
720	29	51.8	2261	2	US-09-032-438C-118	Sequence 118, App	793	28	50.0	38	2	US-08-854-050-218	Sequence 218, App
721	29	51.8	3542	2	US-10-087-013-2	Sequence 2, Appli	794	28	50.0	38	2	US-09-430-323-218	Sequence 218, App
722	28.5	50.9	82	2	US-09-471-276-1563	Sequence 1563, Ap	795	28	50.0	38	2	US-09-402-181B-337	Sequence 337, App
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724	28.5	50.9	94	2	US-08-976-161-63	Sequence 63, Appl	797	28	50.0	38	2	US-10-054-295-218	Sequence 218, App
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726	28.5	50.9	188	2	US-09-621-976-5325	Sequence 5325, Ap	799	28	50.0	40	2	US-08-905-223-387	Sequence 387, App
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728	28.5	50.9	255	2	US-09-471-276-1074	Sequence 1074, Ap	801	28	50.0	44	2	US-09-973-278-392	Sequence 392, App
729	28.5	50.9	293	2	US-09-152-060-83	Sequence 83, Appl	802	28	50.0	44	2	US-09-288-143-106	Sequence 106, App
730	28.5	50.9	293	2	US-09-852-797-83	Sequence 83, Appl	803	28	50.0	48	2	US-09-270-767-35072	Sequence 35072, A
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732	28.5	50.9	293	2	US-10-058-993-83	Sequence 83, Appl	805	28	50.0	51	2	US-09-621-976-4432	Sequence 4432, Ap
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735	28.5	50.9	296	2	US-09-905-125A-207	Sequence 207, App	808	28	50.0	61	2	US-09-621-976-5270	Sequence 5270, Ap
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738	28.5	50.9	296	2	US-09-903-603A-207	Sequence 207, App	811	28	50.0	63	2	US-09-037-742B-13	Sequence 13, Appl
739	28.5	50.9	296	2	US-09-904-920A-207	Sequence 207, App	812	28	50.0	65	2	US-09-621-976-4188	Sequence 4188, Ap
740	28.5	50.9	296	2	US-09-909-064-207	Sequence 207, App	813	28	50.0	65	2	US-09-270-767-37881	Sequence 37881, A
741	28.5	50.9	296	2	US-09-905-381A-207	Sequence 207, App	814	28	50.0	65	2	US-09-270-767-53098	Sequence 53098, A
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743	28.5	50.9	296	2	US-09-906-646-207	Sequence 207, App	816	28	50.0	67	2	US-09-471-276-1155	Sequence 1155, Ap
744	28.5	50.9	296	2	US-09-852-797-60	Sequence 60, Appl	817	28	50.0	69	2	US-09-547-435-16	Sequence 16, Appl
745	28.5	50.9	296	2	US-09-904-462-207	Sequence 207, App	818	28	50.0	71	1	US-08-616-732A-27	Sequence 27, Appl
746	28.5	50.9	296	2	US-09-902-736A-207	Sequence 207, App	819	28	50.0	71	2	US-09-037-742B-27	Sequence 27, Appl
747	28.5	50.9	296	2	US-09-853-161-60	Sequence 60, Appl	820	28	50.0	74	2	US-09-621-976-5993	Sequence 5993, Ap
748	28.5	50.9	296	2	US-09-906-722A-207	Sequence 207, App	821	28	50.0	81	2	US-09-270-767-46642	Sequence 46642, A
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ALIGNMENTS

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RESULT 1
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; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
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; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347,878C

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; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human thymidylate synthase protein sequence
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: D00596/GenBank
US-09-347-878-30

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Best Local Similarity 100.0%; Pred. No. 0.16;
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; GENERAL INFORMATION:
; APPLICANT: Bertino, Joseph R.
; APPLICANT: Banerjee, Debabrata
; APPLICANT: Tong, Youzhi
; APPLICANT: Liu-Chen, Xinyue
; TITLE OF INVENTION: Mutants of Thymidylate Synthase and Uses Thereof
; FILE REFERENCE: D5978
; CURRENT APPLICATION NUMBER: US/09/367,007C
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/US98/02145
; PRIOR FILING DATE: 1998-01-03
; NUMBER OF SEQ ID NOS: 39
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; ORGANISM: Homo sapiens
; FEATURE:
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US-09-367-007C-39

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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necessary bio-DNA
report

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; NUMBER OF SEQ ID NOS: 207012
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10160

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31795

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RESULT 6
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; Sequence 1, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-757-669A-1

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RESULT 7
US-09-230-637-22
; Sequence 22, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpes-like virus
US-09-230-637-22

Query Match      91.1%; Score 51; DB 2; Length 337;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
        |||||
DB      213 LMALPPCHAL 222

RESULT 8
US-09-230-371A-1
; Sequence 1, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
```

```
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-1

Query Match          91.1%; Score 51; DB 2; Length 337;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
Db 213 LMALPPCHLL 222

RESULT 9
US-09-230-637-32
; Sequence 32, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 290
; TYPE: PRT
; ORGANISM: H. ateles
US-09-230-637-32

Query Match          85.7%; Score 48; DB 2; Length 290;
Best Local Similarity 88.9%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 167 MALPPCHVL 175

RESULT 10
US-09-230-637-33
; Sequence 33, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
```

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; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Varicella-zoster virus
US-09-230-637-33

Query Match          85.7%; Score 48; DB 2; Length 301;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
Db 177 LMALPPCHTL 186

RESULT 11
US-09-203-895-3
; Sequence 3, Application US/09203895
; Patent No. 6436410
; GENERAL INFORMATION:
; APPLICANT: Krishnan, B. Rajendra
; APPLICANT: Yoder, S. Christine
; APPLICANT: Durtschi, Becky A.
; TITLE OF INVENTION: DNA ENCODING NEOSPORA DIHYDROFOLATE REDUCTASE
; TITLE OF INVENTION: THYMIDYLATE SYNTHASE
; FILE REFERENCE: PC9890A
; CURRENT APPLICATION NUMBER: US/09/203,895
; CURRENT FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 60/067,507
; EARLIER FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: 60/095,213
; EARLIER FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Neospora caninum
US-09-203-895-3

Query Match          83.9%; Score 47; DB 2; Length 612;
Best Local Similarity 88.9%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 486 MALPPCHLL 494

RESULT 12
US-09-134-001C-3194
; Sequence 3194, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3194
; LENGTH: 322
```

; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3194

Query Match 82.1%; Score 46; DB 2; Length 322;
Best Local Similarity 77.8%; Pred. No. 6.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | :
Db 200 MALPPCHTM 208

RESULT 13
US-09-107-532A-6145
; Sequence 6145, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 324 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...324
; SEQUENCE DESCRIPTION: SEQ ID NO: 6145:
US-09-107-532A-6145

Query Match 82.1%; Score 46; DB 2; Length 324;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | :
Db 201 MALPPCHTM 209

RESULT 14
US-09-134-000C-4346
; Sequence 4346, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4346
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4346

Query Match 82.1%; Score 46; DB 2; Length 325;
Best Local Similarity 77.8%; Pred. No. 6.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | :
Db 202 MALPPCHTM 210

RESULT 15
US-09-083-541-3
; Sequence 3, Application US/09083541
; Patent No. 6323390
; GENERAL INFORMATION:
; APPLICANT: WU, Xue-Ru
; APPLICANT: SUN, Turg-rten
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR HUMAN
; BLADDER CANCER
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,541
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/969,315
; FILING DATE: 13-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/907,800
; FILING DATE: 08-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/464,961
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: WU=42
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-083-541-3

Query Match 78.6%; Score 44; DB 2; Length 44;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8
Db 19 LIALPPCH 26

RESULT 16
US-08-907-800A-2
; Sequence 2, Application US/08907800A
; Patent No. 6001646
; GENERAL INFORMATION:
; APPLICANT: SUN, Tung-Tien
; TITLE OF INVENTION: METHOD AND VECTOR FOR EXPRESSION AND
; ISOLATION OF BIOLOGICALLY ACTIVE MOLECULES IN URINE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY, ROGER L., P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,800A
; FILING DATE: 08-AUG-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,961
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SUN=9A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-907-800A-2

Query Match 78.6%; Score 44; DB 2; Length 184;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8
Db 45 LIALPPCH 52

RESULT 17
US-08-969-317-2
; Sequence 2, Application US/08969317
```

```
; Patent No. 6277968
; GENERAL INFORMATION:
; APPLICANT: Tung-Tien Sun, Xue-Ru Wu
; TITLE OF INVENTION: Methods of Detecting and Classifying
; TITLE OF INVENTION: Bladder Cancer
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,317
; FILING DATE: herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: NYU-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
US-08-969-317-2

Query Match 78.6%; Score 44; DB 2; Length 184;
Best Local Similarity 87.5%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8
Db 45 LVALPPCH 52

RESULT 18
US-09-540-236-2576
; Sequence 2576, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2576
; LENGTH: 282
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2576

Query Match 78.6%; Score 44; DB 2; Length 282;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
Db 159 VALPPCHTL 167
```


RESULT 19
US-09-328-352-8060
; Sequence 8060, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 1999-06-04
; SEQ ID NO 8060
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8060

Query Match 78.6%; Score 44; DB 2; Length 286;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
:|||||
Db 163 VALPPCHTL 171

RESULT 20
US-09-248-796A-18109
; Sequence 18109, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18109
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18109

Query Match 78.6%; Score 44; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8
:|||||
Db 184 MALPPCH 190

RESULT 21
US-09-230-637-31
; Sequence 31, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; TITLE OF INVENTION: Associated Herpesvirus
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637

; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Herpes simplex
US-09-230-637-31

Query Match 78.6%; Score 44; DB 2; Length 294;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
:|||||
Db 171 MVLPPCHVL 179

RESULT 22
US-09-902-540-14293
; Sequence 14293, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14293
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14293

Query Match 76.8%; Score 43; DB 2; Length 161;
Best Local Similarity 77.8%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
:|||||
Db 38 MKLPPCHVL 46

RESULT 23
US-09-489-039A-14294
; Sequence 14294, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14294
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14294

```
Query Match      71.4%; Score 40; DB 2; Length 118;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 ALPPCHA 9
      |||||:
Db      9 ALPPCHS 15

RESULT 24
US-09-489-039A-10055
; Sequence 10055, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10055
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10055

Query Match      71.4%; Score 40; DB 2; Length 266;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHA 9
      |||||:
Db     143 MALAPCHA 150

RESULT 25
US-09-614-912-8
; Sequence 8, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 351
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; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-614-912-8

Query Match      69.6%; Score 39; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PPCHAL 10
      |||||:
Db     209 PPCHAL 214

RESULT 26
US-08-477-451-12
; Sequence 12, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,451
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0335.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1720 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-451-12

Query Match      66.1%; Score 37; DB 1; Length 1720;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PPCHAL 10
      |||||:
Db     1074 PPCHAI 1079

RESULT 27
US-09-959-392-20
; Sequence 20, Application US/09959392
; Patent No. 6806075
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL JOHN
; APPLICANT: WU, QINGYU
; APPLICANT: YAN, WEI
; TITLE OF INVENTION: CORIN, A SERINE PROTEASE
; FILE REFERENCE: BERLX 74A
; CURRENT APPLICATION NUMBER: US/09/959,392
```

;/ CURRENT FILING DATE: 2001-10-25
;/ PRIOR APPLICATION NUMBER: PCT/EP99/03895
;/ PRIOR FILING DATE: 1999-06-04
;/ PRIOR APPLICATION NUMBER: 09/092,029
;/ PRIOR FILING DATE: 1998-06-05
;/ PRIOR APPLICATION NUMBER: 09/314,967
;/ PRIOR FILING DATE: 1999-05-20
;/ NUMBER OF SEQ ID NOS: 34
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 20
;/ LENGTH: 102
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-09-959-392-20

Query Match 64.3%; Score 36; DB 2; Length 102;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
|||||:
Db 68 ALPPCRL 75

RESULT 28

US-09-087-031E-16
;/ Sequence 16, Application US/09087031E
;/ Patent No. 6479255
;/ GENERAL INFORMATION:
;/ APPLICANT: Rubin, Jeffrey S.
;/ APPLICANT: Finch, Paul
;/ APPLICANT: Aaronson, Stuart
;/ APPLICANT: He, Xi
;/ TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
;/ FILE REFERENCE: 11613.13US11
;/ CURRENT APPLICATION NUMBER: US/09/087,031E
;/ CURRENT FILING DATE: 1998-05-29
;/ PRIOR APPLICATION NUMBER: 09/087,031
;/ PRIOR FILING DATE: 1998-05-29
;/ PRIOR APPLICATION NUMBER: 60/050,417
;/ PRIOR FILING DATE: 1997-06-23
;/ NUMBER OF SEQ ID NOS: 27
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 16
;/ LENGTH: 111
;/ TYPE: PRT
;/ ORGANISM: Rat
US-09-087-031E-16

Query Match 64.3%; Score 36; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
|||||:
Db 68 ALPPCRL 75

RESULT 29

US-10-014-055-5
;/ Sequence 5, Application US/10014055
;/ Patent No. 6884871
;/ GENERAL INFORMATION:
;/ APPLICANT: Luyten, Frank P.
;/ APPLICANT: Hoang, Bang
;/ APPLICANT: Moos, Jr., Malcolm
;/ APPLICANT: Wang, Shouwen
;/ TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
GROWTH INDUCING FRZB PROTEIN
;/ NUMBER OF SEQUENCES: 23
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Knobbe, Martens, Olson & Bear
;/ STREET: 620 Newport Center Drive, 16th Floor

;/ CITY: Newport Beach
;/ STATE: CA
;/ COUNTRY: U.S.A.
;/ ZIP: 92660
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: DOS
;/ SOFTWARE: FastSeq Version 1.5
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/10/014,055
;/ FILING DATE: 07-Dec-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/729,452
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Bartfeld, Neil S.
;/ REGISTRATION NUMBER: 39,901
;/ REFERENCE/DOCKET NUMBER: NIH133.001A
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 619-235-8550
;/ TELEFAX: 619-235-0176
;/ TELEX: <Unknown>
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 111 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-014-055-5

Query Match 64.3%; Score 36; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
|||||:
Db 68 ALPPCRL 75

RESULT 30

US-10-028-051A-5
;/ Sequence 5, Application US/10028051A
;/ Patent No. 6924367
;/ GENERAL INFORMATION:
;/ APPLICANT: Luyten, Frank P.
;/ APPLICANT: Moos, Malcolm J.R.
;/ APPLICANT: Hoang, Bang
;/ APPLICANT: Wang, Shouwen
;/ TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
GROWTH INDUCING FRZB PROTEIN
;/ FILE REFERENCE: NIH133.1CPC1
;/ CURRENT APPLICATION NUMBER: US/10/028,051A
;/ CURRENT FILING DATE: 2001-12-19
;/ PRIOR APPLICATION NUMBER: US 08/822333
;/ PRIOR FILING DATE: 1997-03-20
;/ PRIOR APPLICATION NUMBER: US 08/729,452
;/ PRIOR FILING DATE: 1996-10-11
;/ NUMBER OF SEQ ID NOS: 23
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 5
;/ LENGTH: 111
;/ TYPE: PRT
;/ ORGANISM: Rattus norvegicus
US-10-028-051A-5

Query Match 64.3%; Score 36; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHAL 10
||| :|
Db 68 ALPPCRL 75

RESULT 31

```

RESULT 31
US-09-902-540-15035
; Sequence 15035, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wisland, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15035
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15035

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	Query Match	Best Local Similarity	Matches	7; Conserva
Qy	2	MALPPCHA	9	
Dp	65	MALPPGHA	72	

```
Query Match      64.3%; Score 36; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 1.9e+02;
Matches 7: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

DEC 11 1964

```

RESULT 32
US-08-256-747C-76
; Sequence 76, Application US/08256747C
; Patent No. 6037448
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: GILLAM, Shirley
; APPLICANT: OU, Dawei
; APPLICANT: TINGLE, Aubrey
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,747C
; FILING DATE: 06-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids

```

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-256-747C-76

```

Query Match 64.3%; Score 36; DB 2; Length 257;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels

Qy 3 ALPPCHA 9
Db 121 APPPCHA 127

RESULT 33

```

RESULT 33
US-09-902-540-15709
; Sequence 15709, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15709
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15709

```

```

Query Match
Best Local Similarity
Matches      5; Conser
QY          5 PPFCHAL 10
            |||||:|
Db          80 PPFCHSL 85

```

Query Match 64.3%; Score 36; DB 2; Length 463;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels

RESIT.T 34

RESULT 34
US-08-313-200-1
; Sequence 1, Application US/08313200
; Patent No. 598153
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,200
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 20344-20658.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland(from people with Grave's
TISSUE TYPE: disease)
IMMEDIATE SOURCE:
CLONE: pHTPO-2.8
FEATURE:
NAME/KEY: Peptide
LOCATION: Join(1..3, 456..631)
OTHER INFORMATION: /note= "TPO region within fusion
OTHER INFORMATION: plasmid: TPO(delta4-455)"
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..120
OTHER INFORMATION: /note= "C-terminal truncation:
OTHER INFORMATION: TPO(1-120)"
FEATURE:
NAME/KEY: Region
LOCATION: 1..400
OTHER INFORMATION: /note= "TPO epitopic region within
OTHER INFORMATION: fusion protein: MBP-TPO (AA 1-400)"
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..455
OTHER INFORMATION: /note= "C-terminal truncation-
OTHER INFORMATION: TPO(1-455) or N-terminal half of TPO"
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..631
OTHER INFORMATION: /note= "C-terminal truncation:
OTHER INFORMATION: TPO(1-631)"
FEATURE:
NAME/KEY: Region
LOCATION: 266..281
OTHER INFORMATION: /note= "TPO epitopic or binding
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 376..631
OTHER INFORMATION: /note= "TPO epitopic region within
OTHER INFORMATION: fusion protein: MBP-TPO (AA 376-631)"
FEATURE:
NAME/KEY: Region
LOCATION: Join(455..532, 590..933)
OTHER INFORMATION: /note= "alternatively spliced
OTHER INFORMATION: C-terminus of TPO"
FEATURE:
NAME/KEY: Region
LOCATION: 455..933
OTHER INFORMATION: /note= "TPO C-terminus containing
OTHER INFORMATION: binding region"
FEATURE:
NAME/KEY: Region
LOCATION: 456..631
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 456..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 456..933
OTHER INFORMATION: /note= "TPO region within maltose
OTHER INFORMATION: binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 457..517
OTHER INFORMATION: /note= "non-reactive fragment"
FEATURE:
NAME/KEY: Region
LOCATION: 457..633
OTHER INFORMATION: /note= "TPO region within fusion
OTHER INFORMATION: plasmid pMalTPO"
FEATURE:
NAME/KEY: Region
LOCATION: 465..933
OTHER INFORMATION: /note= "TPO binding region of
OTHER INFORMATION: maltose binding region fusion construct"
FEATURE:
NAME/KEY: Region
LOCATION: 513..633
OTHER INFORMATION: /note= "recombinant TPO"
FEATURE:
NAME/KEY: Region
LOCATION: 517..630
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 517..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 573..633
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 590..611
OTHER INFORMATION: /note= "TPO region within maltose
OTHER INFORMATION: binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 590..615
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Binding-site
LOCATION: 590..675
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 592..613
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:

NAME/KEY: Region
LOCATION: 596..611
OTHER INFORMATION: /note= "TPO region within fusion
OTHER INFORMATION: protein"
FEATURE:
NAME/KEY: Region
LOCATION: 602..615
OTHER INFORMATION: /note= "TPO region containing
OTHER INFORMATION: divergent sequences"
FEATURE:
NAME/KEY: Region
LOCATION: 611..615
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 631..933
OTHER INFORMATION: /note= "TPO binding or epitopic
OTHER INFORMATION: region"
FEATURE:
NAME/KEY: Region
LOCATION: 632..933
OTHER INFORMATION: /note= "TPO region within maltose
OTHER INFORMATION: binding fusion protein"
FEATURE:
NAME/KEY: Region
LOCATION: 633..768
OTHER INFORMATION: /note= "TPO binding or epitopic

Query Match 64.3%; Score 36; DB 1; Length 933;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9
| | | | |
Db 804 AHPPCHA 810

RESULT 35

US-09-251-039-2
; Sequence 2, Application US/09251039
; Patent No. 6528059
; GENERAL INFORMATION:
; APPLICANT: Baker, James R.
; APPLICANT: Koenig, Ronald J.
; APPLICANT: University of Michigan
; TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
; FILE REFERENCE: 203442065801
; CURRENT APPLICATION NUMBER: US/09/251,039
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/313,200
; EARLIER FILING DATE: 1994-11-08
; EARLIER APPLICATION NUMBER: 07/885,656
; EARLIER FILING DATE: 1992-05-19
; EARLIER APPLICATION NUMBER: PCT/US93/03837
; EARLIER FILING DATE: 1993-04-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-251-039-2

Query Match 64.3%; Score 36; DB 2; Length 933;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9
| | | | |
Db 804 AHPPCHA 810

RESULT 36

US-09-949-016-5953
; Sequence 5953, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5953
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5953

Query Match 64.3%; Score 36; DB 2; Length 933;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9
| | | | |
Db 804 AHPPCHA 810

RESULT 37

US-09-949-016-7322
; Sequence 7322, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7322
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7322

Query Match 64.3%; Score 36; DB 2; Length 933;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ALPPCHA 9
| | | | |
Db 804 AHPPCHA 810

RESULT 38

PCT-US93-03837-1
; Sequence 1, Application PC/TUS9303837
; GENERAL INFORMATION:
; APPLICANT: Baker, Jr., James R.

APPLICANT: Koenig, Ronald J.
TITLE OF INVENTION: Thyroid Peroxidase Epitopic Regions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03837
FILING DATE: 19930422
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M.
REGISTRATION NUMBER: 33006
REFERENCE/DOCKET NUMBER: 2115-00658PPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 641-1600
TELEFAX: (313) 641-0270
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Mature
TISSUE TYPE: Thyroid gland (from people with Grave's
IMMEDIATE SOURCE:
CLONE: pTFO-2.8
PUBLICATION INFORMATION:
AUTHORS: Kimura, S.
AUTHORS: Kotani, T.
AUTHORS: McBride, O. W.
AUTHORS: Ueki, K.
AUTHORS: Nakayama, T.
AUTHORS: Ohtaki, S.
AUTHORS: Hirai, K.
TITLES: Human thyroid peroxidase: Complete cDNA and
TITLE: protein sequence, chromosome mapping, and
TITLE: identification of two alternately spliced mRNAs
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 84
PAGES: 5555-5559
DATE: 1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 3048
PCT-US93-03837-1

Query Match 64.3%; Score 36; DB 4; Length 933;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHA 9
DB 804 AHPCHA 810

RESULT 39
US-09-902-540-10395
Sequence 10395, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10395
LENGTH: 956
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-10395

Query Match 64.3%; Score 36; DB 2; Length 956;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 729 VLALPPVHGL 738

RESULT 40
US-08-127-499A-1
Sequence 1, Application US/08127499A
Patent No. 5510284
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-08-127-499A-1

Query Match 64.3%; Score 36; DB 1; Length 992;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHA 9

Db 419 APPPCHA 425

RESULT 41

US-08-482-847-1
; Sequence 1, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-1

Query Match 64.3%; Score 36; DB 1; Length 992;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHA 9

Db 419 APPPCHA 425

RESULT 42

US-10-360-101-162
; Sequence 162, Application US/10360101
; Patent No. 6861236
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 162

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sequence of brain derived acidic fibroblast growth factor (1-24)
US-10-360-101-162

Query Match 62.5%; Score 35; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCH 8

Db 11 APPPCH 16

RESULT 43

US-09-534-638-5
; Sequence 5, Application US/09534638
; Patent No. 6320038
; GENERAL INFORMATION:
; APPLICANT: Panula, Pertti A.J.
; APPLICANT: Brandt, Annika
; APPLICANT: Westerlund, Johanna
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
; TITLE OF INVENTION: for therapy and diagnosis
; FILE REFERENCE: 2530-104
; CURRENT APPLICATION NUMBER: US/09/534,638
; CURRENT FILING DATE: 2000-03-27
; EARLIER APPLICATION NUMBER: 09/365755
; EARLIER FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mouse
US-09-534-638-5

Query Match 62.5%; Score 35; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LPPCH 8

Db 91 LPPCH 95

RESULT 44

US-09-270-767-57195
; Sequence 57195, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57195
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57195

Query Match 62.5%; Score 35; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LPPCH 8
: |||||
Db 186 LPPCH 190

RESULT 45

US-09-949-016-7312
; Sequence 7312, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7312
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7312

Query Match 62.5%; Score 35; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LPPCH 8
: |||||
Db 10 LPPCH 14

RESULT 46

US-09-270-767-39225
; Sequence 39225, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39225
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39225

Query Match 62.5%; Score 35; DB 2; Length 268;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
: |||||
Db 50 IFALPSCHCI 59

RESULT 47

US-09-270-767-54442
; Sequence 54442, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54442
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54442

Query Match 62.5%; Score 35; DB 2; Length 268;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
: |||||
Db 50 IFALPSCHCI 59

RESULT 48

US-09-270-767-32903
; Sequence 32903, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32903
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-32903

Query Match 62.5%; Score 35; DB 2; Length 276;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PPCHAL 10
: |||||
Db 103 PPCHGL 108

RESULT 49

US-09-270-767-48120
; Sequence 48120, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48120
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-48120

Query Match 62.5%; Score 35; DB 2; Length 276;
Best Local Similarity 83.3%; Pred. NO. 3.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PCHAL 10
| | | | |
Db 103 PCHGL 108

RESULT 50
US-09-902-540-16237
; Sequence 16237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16237
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16237

Query Match 62.5%; Score 35; DB 2; Length 281;
Best Local Similarity 85.7%; Pred. NO. 3.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHA 9
| | | | |
Db 201 ALPACHA 207

Search completed: February 17, 2006, 02:45:24
Job time : 60 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:40:31 ; Search time 38 Seconds
(without alignments)
25.320 Million cell updates/sec

Title: US-10-734-049B-188
Perfect score: 56
Sequence: 1 LMALPPCHAL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	56	100.0	307	1 YXNST	thymidylate synth
2	56	100.0	307	2 S53715	thymidylate synth
3	56	100.0	213	1 YXHUT	thymidylate synth
4	52	92.9	264	2 G81050	thymidylate synth
5	52	92.9	264	2 A81825	thymidylate synth
6	52	92.9	264	2 D83602	thymidylate synth
7	49	87.5	314	2 AB1309	thymidylate synth
8	49	87.5	314	2 AB1681	thymidylate synth
9	48	85.7	263	2 C70881	probable thya prot
10	48	85.7	264	1 S35239	thymidylate synth
11	48	85.7	264	2 A12827	thymidylate synth
12	48	85.7	264	2 AB3328	thymidylate synth
13	48	85.7	266	2 A87099	thymidylate synth
14	48	85.7	279	2 G97605	hypothetical prote
15	48	85.7	279	2 C87512	thymidylate synth
16	48	85.7	290	1 SYBEAT	thymidylate synth
17	48	85.7	290	2 T42984	thymidylate synth
18	48	85.7	301	1 SYBE13	thymidylate synth
19	48	85.7	316	1 SYLBT	thymidylate synth
20	48	85.7	518	2 T05277	dihydrofolate redu
21	48	85.7	519	2 E84539	dihydrofolate redu
22	48	85.7	528	2 S35272	dihydrofolate redu
23	48	85.7	530	2 S55683	dihydrofolate redu
24	48	85.7	577	2 T14315	dihydrofolate redu
25	47	83.9	289	2 S55667	thymidylate synth
26	47	83.9	387	2 E75250	thymidylate synth
27	47	83.9	520	1 RDLNLS	dihydrofolate redu
28	47	83.9	520	1 RDLNTZ	dihydrofolate redu
29	47	83.9	583	1 RDZQTB	dihydrofolate redu

30	47	83.9	608	1 RDZQK1	dihydrofolate redu
31	47	83.9	610	2 A46005	dihydrofolate redu
32	47	83.9	623	2 JC6568	dihydrofolate redu
33	46	82.1	318	1 YXSAT3	thymidylate synth
34	46	82.1	318	2 C89920	thymidylate synth
35	46	82.1	462	2 S65570	dihydrofolate redu
36	44	78.6	184	2 T09609	uroplakin II - hum
37	44	78.6	184	2 A54135	uroplakin II prote
38	44	78.6	184	2 JC7839	uroplakin II prote
39	44	78.6	185	2 A49713	uroplakin II prote
40	44	78.6	259	1 YXBYT	thymidylate synth
41	44	78.6	286	1 SYBPT4	thymidylate synth
42	44	78.6	294	1 SYBEHS	thymidylate synth
43	44	78.6	297	1 YXUNTP	thymidylate synth
44	44	78.6	315	1 YXCKTA	thymidylate synth
45	44	78.6	328	2 S73842	thymidylate synth
46	44	78.6	521	2 T01684	dihydrofolate redu
47	44	78.6	625	2 T37719	thymidylate synth
48	43	76.8	264	2 G82569	thymidylate synth
49	43	76.8	264	2 B84981	thymidylate synth
50	43	76.8	286	2 B90579	thymidylate synth
51	42	75.0	315	2 T52178	thymidylate synth
52	41	73.2	287	2 A64225	thymidylate synth
53	40	71.4	264	1 SYBSTB	thymidylate synth
54	40	71.4	264	1 SYECT	thymidylate synth
55	40	71.4	264	2 AB0866	thymidylate synth
56	40	71.4	264	2 AE0096	thymidylate synth
57	40	71.4	264	2 C84081	thymidylate synth
58	40	71.4	264	2 F85934	thymidylate synth
59	40	71.4	264	2 D91089	thymidylate synth
60	39	69.6	336	2 T15837	hypothetical prote
61	38	67.9	233	2 A11152	hypothetical prote
62	38	67.9	233	2 AB1512	hypothetical prote
63	38	67.9	292	2 T28399	ORF MSV238 probabl
64	38	67.9	295	2 B83326	conserved hypotet
65	37	66.1	220	2 AH3444	calf thymus ribonu
66	37	66.1	275	2 T04480	acyl-CoA oxidase h
67	36	64.3	307	2 T27061	hypothetical prote
68	36	64.3	358	2 A39467	site-specific DNA-
69	36	64.3	635	2 AC0046	DNA mismatch repai
70	36	64.3	641	2 A45054	probable intercell
71	36	64.3	647	2 JE0337	Frizzled-1 protein
72	36	64.3	933	1 OPHUIT	iodide peroxidase
73	36	64.3	992	1 GNWVR3	structural polypro
74	36	64.3	1063	1 GNWV77	structural polypro
75	36	64.3	4725	1 A44357	dynein heavy chain
76	35	62.5	170	2 T50164	probable cleavage
77	35	62.5	196	2 A30327	corticosterin pre
78	35	62.5	309	2 D84077	homoserine kinase
79	35	62.5	358	2 E71686	hypothetical prote
80	35	62.5	377	2 T34272	hypothetical prote
81	35	62.5	444	2 T22412	hypothetical prote
82	35	62.5	457	2 T21063	hypothetical prote
83	35	62.5	639	1 S45776	uracil transport p
84	35	62.5	926	1 OPGIT	iodide peroxidase
85	35	62.5	1116	2 AC2921	cobalamin biosynth
86	35	62.5	1116	2 D97695	cobN protein homol
87	35	62.5	1650	2 S53457	dominant autoantig
88	35	62.5	4660	2 T42737	gp330 protein proc
89	35	62.5	5376	2 T42215	zonadhesin - mouse
90	34	60.7	140	2 C69269	hypothetical prote
91	34	60.7	190	1 RSHCE	corticosterin pre
92	34	60.7	295	2 S29956	beta-chimerin - ra
93	34	60.7	349	2 T11128	NADH2 dehydrogenas
94	34	60.7	368	2 E87191	o-succinylbenzoic
95	34	60.7	434	2 S69245	RNA polymerase I-a
96	34	60.7	443	2 B53764	beta2-chimerin, ce
97	34	60.7	466	2 A53764	thiamine-phosphate
98	34	60.7	518	1 S44183	Frizzled-7 protein
99	34	60.7	574	2 JE0339	peptidyl-dipectida
100	34	60.7	733	2 AG3561	pleiotropic drug r
101	34	60.7	976	2 S45738	probable retroelem
102	34	60.7	1102	2 A84480	

103	34	60.7	1239	2	G71266	probable ATP-depen	176	32	57.1	439	2	A84431	probable C2H2-type
104	34	60.7	1596	2	A35927	190K DNA-binding p	177	32	57.1	468	2	E70839	probable PB prote
105	33.5	59.8	741	2	B69400	molybdopterin oxid	178	32	57.1	468	2	F84686	hypothetical prote
106	33	58.9	65	2	G35172	cytochrome P450 (c	179	32	57.1	494	2	JX0065	anthranilate synthe
107	33	58.9	109	2	G81244	phnA protein NMB00	180	32	57.1	505	2	T00400	hypothetical prote
108	33	58.9	109	2	F82023	PhnA protein homol	181	32	57.1	538	2	T50606	hypothetical prote
109	33	58.9	137	2	E28705	hypothetical prote	182	32	57.1	565	2	J80338	Frizzled-2 protei
110	33	58.9	183	2	E72459	hypothetical prote	183	32	57.1	566	2	F85214	4-coumarate-CoA li
111	33	58.9	198	2	H83266	probable molybdop	184	32	57.1	566	2	T05038	4-coumarate-CoA li
112	33	58.9	256	2	H82525	uracil-DNA glycosy	185	32	57.1	586	2	A85057	probable transposo
113	33	58.9	294	2	G72706	hypothetical prote	186	32	57.1	632	2	S64786	hypothetical prote
114	33	58.9	311	2	T09656	oryR protein homol	187	32	57.1	655	2	T16538	hypothetical prote
115	33	58.9	311	2	D87164	probable <i>lysR</i> -fami	188	32	57.1	662	2	S62707	NADH2 dehydrogen
116	33	58.9	334	2	C84935	N-acetyl-gamma-glu	189	32	57.1	672	2	T25876	hypothetical prote
117	33	58.9	336	2	H70693	hypothetical prote	190	32	57.1	730	2	B85013	hypothetical prote
118	33	58.9	444	1	B41864	acetyl-CoA-deacety	191	32	57.1	730	2	T10539	GTPase-activator p
119	33	58.9	448	2	T39314	hypothetical prote	192	32	57.1	892	2	T40040	iodide peroxidase
120	33	58.9	499	2	JC6141	beta 1,3-glucanase	193	32	57.1	914	1	S07047	hypothetical prote
121	33	58.9	618	2	T42664	hypothetical prote	194	32	57.1	918	2	G85929	hypothetical prote
122	33	58.9	623	2	S55652	transcription cont	195	32	57.1	918	2	S20550	sensor-regulator p
123	33	58.9	655	2	A40675	nuclear envelope p	196	32	57.1	918	2	F91084	sensor-regulator p
124	33	58.9	656	2	S55262	UV-endonuclease -	197	32	57.1	943	2	T03306	PSD-95/SAP90-asso
125	33	58.9	688	2	B65005	hypothetical prote	198	32	57.1	1023	2	T30257	IGF Fc binding pro
126	33	58.9	688	2	H91029	probable peptidase	199	32	57.1	1043	2	D84900	hypothetical prote
127	33	58.9	688	2	A85874	probable peptidase	200	32	57.1	1170	2	A81368	probable 2-acylgly
128	33	58.9	749	2	A95953	probable bifunctio	201	32	57.1	1281	2	JC5368	dynactin 1 - mouse
129	33	58.9	1129	2	T42732	A-kinase anchoring	202	32	57.1	1283	2	T18939	hypothetical prote
130	33	58.9	1174	1	A43736	creatine kinase (E	203	32	57.1	1325	2	S16129	dyscin-associated
131	33	58.9	1224	2	T26377	hypothetical prote	204	32	57.1	2416	2	T13825	adenomatous polyo
132	33	58.9	1670	2	T06754	DNA-directed RNA p	205	32	57.1	2559	2	T09144	probable guanine n
133	32	57.1	72	2	S49021	retinoic acid rece	206	31.5	56.2	918	2	AI0860	sensor protein [im
134	32	57.1	74	2	S13515	retinoic acid rece	207	31	55.4	24	2	B44008	lethal peptide I -
135	32	57.1	89	2	S13517	retinoic acid rece	208	31	55.4	24	2	A44008	lethal peptide II
136	32	57.1	96	2	T03290	probable lipid tra	209	31	55.4	38	2	T37138	hypothetical prote
137	32	57.1	141	2	A83275	hypothetical cytos	210	31	55.4	43	2	CJ1126	hypothetical prote
138	32	57.1	143	2	S58006	probable olfactory	211	31	55.4	88	2	CJ1126	major allergen cha
139	32	57.1	154	1	QOVLCF	gene X protein - h	212	31	55.4	98	1	KRSHH4	keratin high-sulfu
140	32	57.1	171	2	T28000	hypothetical prote	213	31	55.4	98	2	I47086	BII184 high-sulfu
141	32	57.1	175	2	T52143	auxin-induced prot	214	31	55.4	105	2	E71153	hypothetical prote
142	32	57.1	178	2	T28045	hypothetical prote	215	31	55.4	109	1	D42409	biphenyl dioxygena
143	32	57.1	182	2	A53803	dihydrofolate redu	216	31	55.4	109	1	E41858	biphenyl dioxygena
144	32	57.1	224	2	AD1114	thiamin biosynthes	217	31	55.4	113	2	T36789	hypothetical prote
145	32	57.1	224	2	AE1475	thiamin biosynthes	218	31	55.4	117	2	T49382	hypothetical prote
146	32	57.1	236	2	I59323	apolipoprotein B m	219	31	55.4	120	2	S50867	4E-BP2 protei
147	32	57.1	257	2	T35726	probable cobalt tr	220	31	55.4	122	2	T49462	hypothetical prote
148	32	57.1	261	2	S63604	homeobox protein G	221	31	55.4	139	2	B82865	conserved hypothet
149	32	57.1	262	2	T43986	v-cyclin - ateline	222	31	55.4	146	2	E95363	protein [imported
150	32	57.1	264	2	F72714	hypothetical prote	223	31	55.4	148	2	AF2547	hypothetical prote
151	32	57.1	273	2	I48187	gene Nxx2.2 protei	224	31	55.4	149	2	B48566	cysteine proteinas
152	32	57.1	273	2	JC4634	vertebrate NK-2 ho	225	31	55.4	158	2	B96496	unknown protein, 5
153	32	57.1	275	2	A82578	glycerol uptake fa	226	31	55.4	162	2	A45362	corticolliberin pre
154	32	57.1	292	2	D85863	probable regulator	227	31	55.4	170	2	S44881	ZC262.4 protei
155	32	57.1	292	2	B91019	probable transcrip	228	31	55.4	181	2	S22990	zein, 27K - maize
156	32	57.1	327	2	JT0584	deoxyribonuclease	229	31	55.4	186	2	T34664	methyated-DNA-[pr
157	32	57.1	337	2	AI2360	hypothetical prote	230	31	55.4	190	2	AF1010	conserved hypothet
158	32	57.1	341	2	S51766	dioxygenase - eggp	231	31	55.4	190	2	D89592	hypothetical prote
159	32	57.1	343	2	T02071	glycerolaldehyde-3-p	232	31	55.4	190	2	H91147	hypothetical prote
160	32	57.1	343	2	D89605	protein F18G5.3 (i	233	31	55.4	190	2	E65120	hypothetical prote
161	32	57.1	352	2	H81165	modification methy	234	31	55.4	218	2	G82591	hypothetical prote
162	32	57.1	353	1	A34933	glycoprotein-fuoco	235	31	55.4	223	1	ZM2M19	glutelin 2 precurs
163	32	57.1	356	2	D65096	hypothetical 40.1	236	31	55.4	224	2	T33855	hypothetical prote
164	32	57.1	356	2	H85968	hypothetical prote	237	31	55.4	229	2	JC4269	apolipoprotein B m
165	32	57.1	356	2	A98124	hypothetical prote	238	31	55.4	229	2	JC4269	apolipoprotein B m
166	32	57.1	362	2	B86382	probable zinc fing	239	31	55.4	229	2	I59577	apolipoprotein B m
167	32	57.1	365	2	B39467	site-specific DNA-	240	31	55.4	230	2	T37811	very hypohetical
168	32	57.1	372	2	S77549	pata2 protein - Sy	241	31	55.4	236	2	A53853	apolipoprotein B m
169	32	57.1	400	2	A46297	beta-1,6-N-acetylgl	242	31	55.4	241	2	S74620	hypohetical prote
170	32	57.1	413	1	S39554	histidine decarbox	243	31	55.4	243	2	H85950	hypohetical prote
171	32	57.1	413	1	A34888	transcription fact	244	31	55.4	243	2	E91105	hypohetical lipop
172	32	57.1	419	2	F96704	hypothetical prote	245	31	55.4	256	2	A60533	tumor-associated a
173	32	57.1	435	2	G90700	probable uracil tr	246	31	55.4	262	2	T31305	4-hydroxy-2-oxoval
174	32	57.1	435	2	B85551	probable transport	247	31	55.4	278	2	G44796	F0968.6 protei
175	32	57.1	435	2	H64782	probable membrane	248	31	55.4	290	2	S85045	probable hydrolase

249	31	55.4	291	2	AF0123	probable antigenic	322	31	55.4	3068	1	A44062	genome polyprotein
250	31	55.4	298	2	T27090	hypothetical prote	323	30.5	54.5	384	2	F32252	gene III protein -
251	31	55.4	299	2	T25610	hypothetical prote	324	53.6	53.6	16	2	A54877	alpha-conotoxin Pn
252	31	55.4	303	2	G71109	hypothetical prote	325	30	53.6	39	1	A48523	margatoxin [valida
253	31	55.4	311	2	D82786	thiamin biosynthes	326	30	53.6	45	2	T25203	hypothetical prote
254	31	55.4	315	2	T26673	hypothetical prote	327	30	53.6	51	2	AF3350	hypothetical prote
255	31	55.4	316	2	T08807	mitochondrial proc	328	30	53.6	78	2	E90319	hypothetical prote
256	31	55.4	321	2	T46544	cyclase [imported]	329	30	53.6	91	2	T29796	hypothetical prote
257	31	55.4	326	2	S56534	hypothetical 36.9K	330	30	53.6	98	1	PCRT	pancreatic hormone
258	31	55.4	338	2	E98337	probable zinc-bind	331	30	53.6	109	2	S28735	hypothetical prote
259	31	55.4	338	2	AE3945	zinc-binding dehyd	332	30	53.6	127	2	AG2241	hypothetical prote
260	31	55.4	345	2	S04280	psbA intron 1 prot	333	30	53.6	136	2	T19990	hypothetical prote
261	31	55.4	354	2	S25267	cysteine proteinas	334	30	53.6	143	2	S58071	probable olfactory
262	31	55.4	358	1	WMBE38	infected cell prot	335	30	53.6	147	2	T49706	hypothetical prote
263	31	55.4	362	2	T04920	polygalacturonase	336	30	53.6	154	2	A40323	Rodletless protein
264	31	55.4	362	2	T02057	fructose-bisphosph	337	30	53.6	177	2	G71360	methylated-DNA-lpr
265	31	55.4	362	2	T05457	probable menE - My	338	30	53.6	186	2	T03570	hypothetical prote
266	31	55.4	367	1	W0HU	alpha-2-HS-glycopr	339	30	53.6	208	1	JCI409	heparin-binding EG
267	31	55.4	370	2	T11849	gibberellin 20-oxi	340	30	53.6	219	2	G71343	hypothetical prote
268	31	55.4	374	2	H87575	hypothetical prote	341	30	53.6	228	2	T45553	cytochrome-c oxida
269	31	55.4	383	2	S54213	flagellar biosynth	342	30	53.6	235	2	C82530	hypothetical prote
270	31	55.4	389	2	C82987	probable MFS trans	343	30	53.6	249	2	C81180	tRNA (guanine-N1) -
271	31	55.4	395	2	E90438	hypothetical prote	344	30	53.6	249	2	A81924	probable tRNA (gua
272	31	55.4	395	2	H72654	hypothetical prote	345	30	53.6	256	2	D82369	thiamin biosynthes
273	31	55.4	403	2	A26371	sex steroid-bindin	346	30	53.6	259	2	B72505	hypothetical prote
274	31	55.4	412	2	D86203	hypothetical prote	347	30	53.6	267	2	T37862	dmal protein - fis
275	31	55.4	414	2	E85204	hypothetical prote	348	30	53.6	269	2	T22778	hypothetical prote
276	31	55.4	435	2	T26558	probable isocitrat	349	30	53.6	276	2	T48843	halorhodopsin [val
277	31	55.4	441	2	T23461	hypothetical prote	350	30	53.6	276	2	T48842	halorhodopsin [sm
278	31	55.4	448	2	H70947	hypothetical prote	351	30	53.6	293	2	AC3495	probable enoyl-CoA
279	31	55.4	456	2	A71501	probable hexosphos	352	30	53.6	294	2	S13141	hypothetical prote
280	31	55.4	464	2	T46333	hypothetical prote	353	30	53.6	295	2	T08183	hypothetical prote
281	31	55.4	476	2	S36513	L2 protein - human	354	30	53.6	295	2	JEO174	frizzled protein-2
282	31	55.4	477	2	D75469	probable regulator	355	30	53.6	299	2	H87567	hypothetical prote
283	31	55.4	487	2	E70508	hypothetical prote	356	30	53.6	306	2	S67131	hypothetical prote
284	31	55.4	489	1	S36390	mitochondrial prote	357	30	53.6	316	2	AB2868	UDP-hexose transfe
285	31	55.4	492	2	T01235	hypothetical prote	358	30	53.6	316	2	F97644	hypothetical prote
286	31	55.4	499	2	H86148	hypothetical prote	359	30	53.6	316	2	T31880	hypothetical prote
287	31	55.4	518	1	S27381	probable serine/th	360	30	53.6	320	2	T01874	hypothetical prote
288	31	55.4	524	2	T06134	hypothetical prote	361	30	53.6	324	2	T18790	hypothetical prote
289	31	55.4	530	2	T32812	hypothetical prote	362	30	53.6	326	2	T10600	hypothetical prote
290	31	55.4	531	2	T22021	hypothetical prote	363	30	53.6	326	2	A41855	activator-regulato
291	31	55.4	556	2	AE6718	squalene-hopene cy	364	30	53.6	327	2	F90180	sun (fmu) protein
292	31	55.4	593	2	AB0046	probable N-acetyl m	365	30	53.6	334	2	JC6082	proximal sequence
293	31	55.4	603	2	JC1282	insulin-like growt	366	30	53.6	334	2	S29128	N-chimerin - rat
294	31	55.4	605	2	T71630	metalloproteinase	367	30	53.6	342	2	D95906	probable transcrip
295	31	55.4	605	2	AG0123	probable antigenic	368	30	53.6	348	2	S52720	homeobox protein G
296	31	55.4	623	2	H96766	unknown protein F2	369	30	53.6	353	2	B96767	unknown protein F2
297	31	55.4	626	2	AE0123	probable antigenic	370	30	53.6	364	2	AG2537	cysteine synthase
298	31	55.4	629	2	C87048	probable ABC trans	371	30	53.6	369	2	I49280	interleukin-2 rece
299	31	55.4	653	2	E72080	penicillin-binding	372	30	53.6	370	2	S77011	mercuric resistanc
300	31	55.4	653	2	A86543	transglycolase/tra	373	30	53.6	396	1	TRYXB4	alpha-lytic protei
301	31	55.4	666	2	T10567	probable serine/th	374	30	53.6	398	2	F69266	3-ketoacyl-CoA thi
302	31	55.4	695	2	T40168	hypothetical prote	375	30	53.6	406	2	C43664	tryptophan synthas
303	31	55.4	753	2	A27041	tyrosine kinase-re	376	30	53.6	406	2	A47696	acetylaminase - Myc
304	31	55.4	760	2	F86387	probable Pto kinas	377	30	53.6	410	2	F87688	tryptophan synthas
305	31	55.4	781	2	AC2086	hypothetical prote	378	30	53.6	415	2	H86204	probable phosphoes
306	31	55.4	815	2	H96494	protein FYE22.2 li	379	30	53.6	427	2	I38909	damage-specific DN
307	31	55.4	882	2	A39030	androgen-binding p	380	30	53.6	461	2	A32008	site-specific DNA-
308	31	55.4	901	2	A49227	sialidase - Actino	381	30	53.6	476	2	H82177	conserved hypotet
309	31	55.4	907	2	H95973	probable two-compo	382	30	53.6	482	2	F71969	hypothetical prote
310	31	55.4	913	1	VGBEPS	glycoprotein gII p	383	30	53.6	495	2	S32179	tniQ protein homol
311	31	55.4	913	2	S20590	exo-alpha-sialidas	384	30	53.6	496	2	D75293	uracil permease -
312	31	55.4	914	1	JN0550	iodide peroxidase	385	30	53.6	513	2	A69831	probable acid-CoA
313	31	55.4	1049	2	T42045	beta transducin-li	386	30	53.6	513	2	T41011	hypothetical prote
314	31	55.4	1184	2	A55184	fibulin-2 precurs	387	30	53.6	515	2	F96011	probable long-chai
315	31	55.4	1247	2	E88557	protein F5H2.6 [i	388	30	53.6	528	2	S22811	hypothetical prote
316	31	55.4	1339	2	JC4387	epidermal growth f	389	30	53.6	531	2	D70946	NADH2 dehydrogenas
317	31	55.4	1342	2	AC6223	kinase-related tra	390	30	53.6	540	2	T47858	hypothetical prote
318	31	55.4	1493	2	T10757	MAP kinase kinase	391	30	53.6	573	2	C95856	probable dihydroxy
319	31	55.4	1596	2	A41216	guanine nucleotide	392	30	53.6	579	2	JC7170	fimbria-like 71 K
320	31	55.4	2318	2	S45306	notch 3 protein -	393	30	53.6	581	2	S03540	gene frizzled prot
321	31	55.4	2326	2	T29140	hypothetical prote	394	30	53.6	583	2	T11210	lisocitrate dehydr

395 30 53.6 586 2 A12065
 396 30 53.6 589 2 T01709
 397 30 53.6 592 2 S25705
 398 30 53.6 593 2 A1011
 399 30 53.6 605 2 A48115
 400 30 53.6 605 2 T01067
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 419 30 53.6 783 1 A38637
 420 30 53.6 783 2 T30644
 421 30 53.6 801 2 H64817
 422 30 53.6 806 2 A1960
 423 30 53.6 823 2 F64526
 424 30 53.6 850 2 T51541
 425 30 53.6 867 2 T14777
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 427 30 53.6 922 2 D75615
 428 30 53.6 964 2 T1547
 429 30 53.6 966 1 T18VBB
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 433 30 53.6 1191 2 AF2501
 434 30 53.6 1195 2 S76592
 435 30 53.6 1299 2 T18398
 436 30 53.6 1308 2 T18408
 437 30 53.6 1342 2 T18405
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 442 30 53.6 2176 2 T39188
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 444 30 53.6 2274 2 T30258
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 446 30 53.6 4957 2 T03455
 447 30 53.6 5262 2 T03454
 448 29.5 52.7 101 2 S04034
 449 29.5 52.7 275 2 A82257
 450 29.5 52.7 394 2 T34708
 451 29 51.8 25 S52359
 452 29 51.8 29 T17079
 453 29 51.8 31 2 B42176
 454 29 51.8 59 2 A3601
 455 29 51.8 63 2 I32277
 456 29 51.8 63 2 G82064
 457 29 51.8 63 2 T31143
 458 29 51.8 64 2 S75543
 459 29 51.8 98 2 G91248
 460 29 51.8 101 2 B84708
 461 29 51.8 105 2 C87324
 462 29 51.8 107 2 A64643
 463 29 51.8 107 2 C72623
 464 29 51.8 111 2 C72514
 465 29 51.8 114 2 H81960
 466 29 51.8 115 2 A81017
 467 29 51.8 127 2 F70910

hypotheoretical prote
 hypotheoretical prote
 Ig mu chain - shee
 isocitrate dehydro
 transcription fact
 transcription fact
 high affinity sulf
 hypotheoretical prote
 dynein light chain
 catechol oxidase (
 probable CHP-rich
 En/spm-like transp
 adhesion-type prot
 Kallmann syndrome
 conserved hypothe
 excinuclease ABC c
 probable protein-t
 telomere-associate
 Down-syndrome-crit
 telomere-associate
 hypotheoretical prote
 DNA helicase/prima
 origin binding pro
 Ras interactor RIN
 hypotheoretical prote
 probable membrane
 hypotheoretical prote
 adenine/cytosine D
 hypotheoretical prote
 protein kinase ABC c
 excinuclease ABC c
 hypotheoretical prote
 RNA la protein - b
 probable helicase
 hypotheoretical prote
 adenyate cyclase
 WD-repeat protein
 5-methyltetrahydro
 latrophilin-3, spl
 latrophilin-3, spl
 latrophilin-3, spl
 latrophilin-3, spl
 probable membrane
 latrophilin-3, spl
 latrophilin-3, spl
 probable US snRNP-
 SEC16 protein - ye
 adenomatous polyo
 transmembrane prot
 ALR protein - huma
 ALR protein - huma
 probable membrane
 oxidoreductase, sh
 hypotheoretical prote
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 NADH2 dehydrogenas
 insulin-like growt
 lysine-trna ligase
 platelet-derived g
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 conserved hypothe
 isoprenylated prot
 hypotheoretical prote
 probable secretion
 10K zein precursor
 isoprenylated prot
 crtk protein - rho
 O6-methylguanine-D
 probable DNA-direc
 collagen alpha 3(I
 probable membrane
 hypotheoretical prote
 hypotheoretical prote
 troic protein - co
 hypotheoretical 20.6K
 hypotheoretical prote
 hypotheoretical prote
 peptidoglycan-asso
 ubiquinol-cytochro
 hypotheoretical prote
 methylated-DNA-lpr
 hypotheoretical prote
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 USF2 protein mou
 protein disulfide-
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 arginine ABC trans
 hypotheoretical prote
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 chalcone isomerase
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 probable molecular
 ubiquinol-cytochro
 probable chaperone
 probable chaperone
 sulfolipid biosynt
 probable fibrial
 collagen alpha 3(I
 fumarate reductase
 hypotheoretical prote
 homeotic protein e
 aquaporin Tjp18 -
 water channel prot
 hemolysin [impor
 14-3-3 brain prote
 D-2-chloropropioni
 pyrroline-5-carbox
 hypotheoretical prote
 conserved hypothe
 Phox2 homeodomain
 voltage-dependent
 hypotheoretical prote
 hypotheoretical prote
 probable peptidase
 hypotheoretical prote
 transcription fact
 beta lactamase pre
 protein K04A8.2 [i
 homeotic protein H
 positive regulator
 transketolase (EC
 phytoene synthase
 protein K04G7.10 [
 probable alcohol d
 hypotheoretical prote

541	29	51.8	337	2	A12144	hypothetical prote	614	29	51.8	583	2	T50103	probable oxidoredu
542	29	51.8	338	2	I52608	glycoprotein D - h	615	29	51.8	585	2	E70930	hypothetical prote
543	29	51.8	339	1	TVBV2A	casein kinase II (616	29	51.8	589	2	A34341	poly(3-hydroxybuty
544	29	51.8	339	2	AG0799	probable transcrip	617	29	51.8	589	2	JG0196	protein kinase DFR
545	29	51.8	344	2	T28839	hypothetical prote	618	29	51.8	605	2	A82381	conserved hypothet
546	29	51.8	346	2	A55111	transcription fact	619	29	51.8	616	2	I38231	S-laminin - human
547	29	51.8	346	2	JC7638	upstream stimulat	620	29	51.8	620	2	A61086	dopamine beta-mono
548	29	51.8	347	1	OXPCDA	D-amino-acid oxida	621	29	51.8	621	2	JC1346	protein kinase DFR
549	29	51.8	351	2	T11794	NADH2 dehydrogenas	622	29	51.8	629	2	JG0195	hypothetical prote
550	29	51.8	353	2	T35531	Rieske iron-sulfur	623	29	51.8	631	2	T20037	metalloproteinase
551	29	51.8	366	2	B36919	hypothetical prote	624	29	51.8	633	2	S61435	hypothetical prote
552	29	51.8	367	2	G71803	hypothetical prote	625	29	51.8	633	2	S07824	hypothetical prote
553	29	51.8	369	2	A42565	interleukin-2 rece	626	29	51.8	639	2	S70126	prostaglandin tran
554	29	51.8	370	2	H69291	conserved hypothet	627	29	51.8	643	2	A41120	conserved hypothet
555	29	51.8	371	2	A86264	protein F3P19.3 (i	628	29	51.8	646	2	H71378	metalloproteinase
556	29	51.8	373	2	A55718	interleukin-2 rece	629	29	51.8	649	2	S42894	hypothetical prote
557	29	51.8	373	2	B75276	DNA-binding respon	630	29	51.8	663	2	S21912	BRcore-Q1-z1 prote
558	29	51.8	375	2	S63685	neuropeptide Y rec	631	29	51.8	664	1	TNBE70	70.5K alpha trans-
559	29	51.8	386	2	D96918	probable SAM depen	632	29	51.8	667	2	S63587	gene pacc protein
560	29	51.8	388	2	S41940	oligogalacturonide	633	29	51.8	667	2	E84018	two-component sens
561	29	51.8	396	2	AB1796	efflux protein hom	634	29	51.8	676	2	T40772	hypothetical prote
562	29	51.8	396	2	AB1421	efflux protein hom	635	29	51.8	684	2	F83375	hypothetical prote
563	29	51.8	397	2	D83311	conserved hypothet	636	29	51.8	688	2	T37923	hypothetical prote
564	29	51.8	397	2	E69094	conserved hypothet	637	29	51.8	689	2	S60306	BPF-1 protein - pa
565	29	51.8	400	2	T28024	hypothetical prote	638	29	51.8	704	2	S21911	BRcore-NS-z3 prote
566	29	51.8	402	2	T52356	related to GTP-bin	639	29	51.8	728	2	S21913	BRcore-TNT1-Q1-z1
567	29	51.8	406	2	AC2579	tryptophan syntha	640	29	51.8	729	2	T51896	probable translati
568	29	51.8	406	2	AF0240	imidazolonepropion	641	29	51.8	729	2	D72079	conserved hypothet
569	29	51.8	406	2	T46988	hypothetical prote	642	29	51.8	729	2	H85544	CT283 hypothetical
570	29	51.8	406	2	G96497	hypothetical prote	643	29	51.8	738	2	T41730	hypothetical prote
571	29	51.8	406	2	H84590	hypothetical prote	644	29	51.8	739	2	H85245	VPI like protein I
572	29	51.8	417	2	B97361	tryptophan syntha	645	29	51.8	739	2	T05163	hypothetical prote
573	29	51.8	428	2	I51680	Xwt-8b - African	646	29	51.8	752	2	T48574	hypothetical prote
574	29	51.8	433	2	B72025	flagellum-specific	647	29	51.8	752	2	H96603	unknown protein F1
575	29	51.8	433	2	A81513	virulence ATPase,	648	29	51.8	786	2	A47546	triacylglycerol li
576	29	51.8	433	2	H86597	flagellum-specific	649	29	51.8	789	2	A39564	transcription repr
577	29	51.8	438	2	T75587	probable chalcone	650	29	51.8	792	2	C82767	phenylalaninyl-CNA
578	29	51.8	440	2	T11319	NADH2 dehydrogenas	651	29	51.8	820	2	T32908	hypothetical prote
579	29	51.8	444	2	F85648	hypothetical prote	652	29	51.8	837	2	T00355	hypothetical prote
580	29	51.8	444	2	E90788	probable outer mem	653	29	51.8	838	2	T20125	hypothetical prote
581	29	51.8	455	2	S33033	hypothetical prote	654	29	51.8	871	2	G86586	DNA topoisomerase
582	29	51.8	456	2	D84651	hypothetical prote	655	29	51.8	871	2	D72038	DNA topoisomerase
583	29	51.8	466	2	H69153	asparagine synthas	656	29	51.8	905	2	T26430	hypothetical prote
584	29	51.8	471	2	T39571	protein T6D22.12 I	657	29	51.8	913	2	A86237	protein F1AN23.15
585	29	51.8	473	2	C86215	protein T6D22.12 I	658	29	51.8	916	2	H72372	excinnuclease ABC c
586	29	51.8	479	2	T44326	hypothetical prote	659	29	51.8	943	2	T16768	hypothetical prote
587	29	51.8	480	2	T18905	hypothetical prote	660	29	51.8	953	2	I48078	CHO1 antigen - Chi
588	29	51.8	482	2	T17250	hypothetical prote	661	29	51.8	961	2	AE2270	excinnuclease ABC c
589	29	51.8	490	2	S53639	protein kinase cik	662	29	51.8	978	2	T16948	hypothetical prote
590	29	51.8	490	2	S70352	protein kinase cik	663	29	51.8	982	2	E88465	protein B0244.6 (i
591	29	51.8	498	2	T51430	dolichyl-phosphate	664	29	51.8	984	2	S14382	hypothetical prote
592	29	51.8	499	2	T45946	probable protein-k	665	29	51.8	998	2	S31735	NAD ADP-ribosyltra
593	29	51.8	505	2	D63382	conserved hypothet	666	29	51.8	1038	2	T02634	rep protein homolo
594	29	51.8	507	2	A86938	probable lysyl-trn	667	29	51.8	1058	2	T30178	mitotic checkpoint
595	29	51.8	511	2	D75540	conserved hypothet	668	29	51.8	1089	2	E81446	carbamoyl-phosphat
596	29	51.8	513	2	H83375	probable glycogen	669	29	51.8	1102	2	T31004	probable mitotic c
597	29	51.8	514	2	S21914	BRcore-z protein -	670	29	51.8	1108	2	A48508	cyclic-nucleotide
598	29	51.8	514	2	H70699	probable ppp prote	671	29	51.8	1112	2	S70522	cyclic nucleotide
599	29	51.8	518	2	T22375	hypothetical prote	672	29	51.8	1120	2	S46111	probable membrane
600	29	51.8	519	2	S78089	G-protein signalin	673	29	51.8	1188	1	NDECKR	type I site-specif
601	29	51.8	519	2	A49367	transducin homolog	674	29	51.8	1193	2	T50729	magnesium-protopor
602	29	51.8	524	2	D84718	probable glutamyl	675	29	51.8	1285	2	T14171	ataxin-2 - mouse
603	29	51.8	530	2	D82063	probable thiamin A	676	29	51.8	1430	2	T12449	hypothetical prote
604	29	51.8	537	2	F97546	hypothetical prote	677	29	51.8	1469	2	T09219	basal transcriptio
605	29	51.8	537	2	AB2766	sulfate permease I	678	29	51.8	1531	2	T48946	hypothetical prote
606	29	51.8	538	2	H86605	acylglycerophospho	679	29	51.8	1612	2	S51243	probable ATPase (E
607	29	51.8	538	2	A72018	Aas bifunctional p	680	29	51.8	1700	2	S08167	Balbani ring 3 pr
608	29	51.8	559	2	T20709	hypothetical prote	681	29	51.8	1770	2	S56221	hypothetical prote
609	29	51.8	561	1	A44128	(N-acetylneuraminy	682	29	51.8	1797	2	A55677	laminin beta-2 cha
610	29	51.8	561	2	JC2447	carboxylesterase (683	29	51.8	1798	2	S53869	laminin beta-2 cha
611	29	51.8	566	2	T34842	probable transfera	684	29	51.8	1801	1	MMETS	laminin beta-2 cha
612	29	51.8	574	2	T00245	reverse transcript	685	29	51.8	1807	2	T30940	vitellogenin - Pim
613	29	51.8	579	2	JC7629	membrane-type friz	686	29	51.8	1822	2	S44849	K12H4.8 protein -

687 29 51.8 1970 2 T03284 myoblast city prot
688 29 51.8 2139 2 S46404 vitellogenin - yel
689 29 51.8 2175 1 S03170 homeotic protein c
690 29 51.8 2201 2 A54774 ATP binding casset
691 29 51.8 3341 1 A42996 genome polyprotein
692 29 51.8 3947 2 T52486 ferrichrome sidero
693 28.5 50.9 230 2 T49555 related to high cy
694 28.5 50.9 276 2 T30594 conserved hypothet
695 28.5 50.9 327 2 D86474 probable RING zinc
696 28.5 50.9 405 2 H71984 probable carboxyno
697 28.5 50.9 415 2 S32932 regulatory protein
698 28.5 50.9 497 2 S22708 homeotic protein e
699 28.5 50.9 555 2 A37181 perforin 1 precurs
700 28 50.0 1310 1 I53597 proline dehydrogen
701 28 50.0 16 2 B54877 alpha-conotoxin Pn
702 28 50.0 32 1 LPEBIT ilvGEDA leader pep
703 28 50.0 32 1 LPECI ilvMEDA operon le
704 28 50.0 32 2 AG0924 ilvMEDA operon at
705 28 50.0 32 2 F86062 ilvMEDA operon lea
706 28 50.0 32 2 E91216 H+-transporting tw
707 28 50.0 60 2 A30160 probable protein t
708 28 50.0 63 2 T41452 hypothetical prote
709 28 50.0 71 2 D87422 hypothetical prote
710 28 50.0 83 1 NPSRI2 neurotoxin I' prec
711 28 50.0 88 2 H30010 hypothetical ORF-9
712 28 50.0 89 2 S72603 hypothetical prote
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714 28 50.0 97 2 AD2171 virulence-associat
715 28 50.0 97 2 B97574 hypothetical prote
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717 28 50.0 101 2 S47414 conserved hypothet
718 28 50.0 102 2 A12630 conserved hypothet
719 28 50.0 106 2 T00722 hypothetical prote
720 28 50.0 110 2 H36602 unknown protein F1
721 28 50.0 110 2 B72730 hypothetical prote
722 28 50.0 113 2 A83631 conserved hypothet
723 28 50.0 118 2 B72524 hypothetical prote
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725 28 50.0 122 2 J65458 high sulfur protei
726 28 50.0 122 2 T46369 hypothetical prote
727 28 50.0 127 2 E84225 hypothetical prote
728 28 50.0 129 2 H75351 conserved hypothet
729 28 50.0 131 2 G82684 hypothetical prote
730 28 50.0 135 2 C98020 cytidine deaminase
731 28 50.0 142 1 S06630 hyperglycemic horm
732 28 50.0 142 2 T03895 hypothetical prote
733 28 50.0 143 1 A60159 interleukin-3 prec
734 28 50.0 144 2 B82423 thioredoxin 2 VCA0
735 28 50.0 146 2 F90337 hypothetical prote
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737 28 50.0 150 2 J01072 10k zein protein -
738 28 50.0 152 1 B24427 interleukin-3 prec
739 28 50.0 152 1 K8SHHC keratin high-sulfu
740 28 50.0 152 2 I47111 high-sulfur wool m
741 28 50.0 152 2 I47109 high-sulfur wool m
742 28 50.0 152 2 I47108 high-sulfur wool m
743 28 50.0 152 2 I47112 high-sulfur wool m
744 28 50.0 152 2 E39925 hypothetical prote
745 28 50.0 155 2 G71369 probable quinoline
746 28 50.0 156 1 K8SHHB keratin high-sulfu
747 28 50.0 156 2 D82799 hypothetical prote
748 28 50.0 157 2 S31078 seed allergen RA5
749 28 50.0 158 2 H75567 hypothetical prote
750 28 50.0 159 2 T48209 hypothetical prote
751 28 50.0 160 2 S47021 ribosomal protein
752 28 50.0 161 2 T26469 hypothetical prote
753 28 50.0 161 2 T11855 DnaJ protein homol
754 28 50.0 162 2 I47107 high-sulfur wool m
755 28 50.0 163 2 D95299 conserved hypothet
756 28 50.0 166 2 A46557 nucleoside-diphosp
757 28 50.0 168 2 B72360 crossover junction
758 28 50.0 169 1 Q0BCA1 cell division inhi
759 28 50.0 169 2 H85622 hypothetical prote

760 28 50.0 169 2 B90759 suppressor of lon
761 28 50.0 172 1 K8SHHA keratin high-sulfu
762 28 50.0 172 2 I47106 high-sulfur wool m
763 28 50.0 173 2 B83504 hypothetical prote
764 28 50.0 174 2 T01486 hypothetical prote
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766 28 50.0 175 2 T34895 hypothetical prote
767 28 50.0 178 1 TVRTSM transforming prote
768 28 50.0 180 2 AD3499 ribosomal-protein-
769 28 50.0 181 2 S75415 probable ribosomal
770 28 50.0 182 1 K8SHHD keratin high-sulfu
771 28 50.0 182 2 I47105 mannose-binding le
772 28 50.0 183 2 S62650 hypothetical prote
773 28 50.0 184 2 F84684 hypothetical prote
774 28 50.0 184 2 H75334 hypothetical prote
775 28 50.0 185 2 A72528 corticosteroid pre
776 28 50.0 187 1 RHRTCE corticosteroid pre
777 28 50.0 188 2 AF2530 hypothetical prote
778 28 50.0 195 2 C75490 hypothetical prote
779 28 50.0 196 2 AG0976 mannitol operon re
780 28 50.0 197 2 A87286 conserved hypothet
781 28 50.0 198 2 A45067 laminin B1 chain v
782 28 50.0 199 2 JT0767 chitin synthase (E
783 28 50.0 200 2 S03811 pss2 protein - Rhi
784 28 50.0 201 2 F65137 hypothetical 21.7
785 28 50.0 204 1 S17289 tumor necrosis fac
786 28 50.0 205 2 T32135 hypothetical prote
787 28 50.0 209 2 C98302 arylesterase (AF04
788 28 50.0 209 2 AE2981 arylesterase [impo
789 28 50.0 210 2 H75599 probable acetyltra
790 28 50.0 212 2 B84337 deoxy-ribose-phosph
791 28 50.0 214 2 B33985 wound-inducible ch
792 28 50.0 215 2 S30169 alkylmercury lyase
793 28 50.0 221 2 J10090 endymnin precursor
794 28 50.0 221 2 A25951 placental lactogen
795 28 50.0 222 2 A26489 hypothetical prote
796 28 50.0 222 2 T23822 probable transcrip
797 28 50.0 222 2 E83615 conserved hypothet
798 28 50.0 223 2 A82139 hypothetical prote
799 28 50.0 223 2 F91210 hypothetical prote
800 28 50.0 223 2 A86057 hypothetical prote
801 28 50.0 223 2 AG3288 2-hydroxy-6-oxo-2,
802 28 50.0 232 2 G87629 hypothetical prote
803 28 50.0 233 2 G83452 heme exporter prot
804 28 50.0 234 2 E86457 porphobilinogen de
805 28 50.0 234 2 B72126 porphobilinogen de
806 28 50.0 241 2 C75361 hypothetical prote
807 28 50.0 241 2 B87337 ada regulatory pro
808 28 50.0 245 2 A43905 sperm outer dense
809 28 50.0 245 2 B82764 hypothetical prote
810 28 50.0 247 2 I48659 outer dense fiber
811 28 50.0 248 2 T48885 water channel prot
812 28 50.0 249 2 A37280 C/EBP-related prot
813 28 50.0 250 2 S71522 outer dense fiber
814 28 50.0 251 2 C97437 hypothetical prote
815 28 50.0 254 2 E82791 conserved hypothet
816 28 50.0 256 2 T45970 hypothetical prote
817 28 50.0 256 2 C91177 hypothetical prote
818 28 50.0 256 2 D86023 hypothetical prote
819 28 50.0 257 2 C64442 hypothetical prote
820 28 50.0 257 2 A71059 hypothetical prote
821 28 50.0 258 2 J01666 transcriptional init
822 28 50.0 259 2 AG2554 hypothetical prote
823 28 50.0 262 2 T04406 14-3-3b protein - r
824 28 50.0 262 2 T04152 GF14-b protein - r
825 28 50.0 262 2 S56100 outer dense fiber
826 28 50.0 263 2 S56101 outer dense fiber
827 28 50.0 263 2 T10535 pssA protein - Rhi
828 28 50.0 264 2 E83284 probable enoyl-CoA
829 28 50.0 264 2 AC0564 conserved hypothet
830 28 50.0 266 2 B83045 hypothetical prote
831 28 50.0 269 2 I50504 nk2.2 protein - ze
832 28 50.0 277 2 D70569 probable lipf prot

833	28	50.0	279	1	I40494	thymidylate synthase	906	28	50.0	403	2	S28144	acetyl-CoA C-acetyl
834	28	50.0	279	1	SYBP3T	thymidylate synthase	907	28	50.0	404	2	S75529	beta ketoacyl-acyl
835	28	50.0	279	2	A97871	hypothetical prote	908	28	50.0	404	2	F82092	aminotransferase,
836	28	50.0	279	2	H71650	coproporphyrinogen	909	28	50.0	410	2	AH2194	pantothenate metab
837	28	50.0	283	2	G01926	insulin promoter f	910	28	50.0	412	2	S76984	hypothetical prote
838	28	50.0	287	2	AH3492	hydroxymethylgluta	911	28	50.0	413	2	F98155	D-alanine dehydrog
839	28	50.0	287	2	S71548	homeotic protein p	912	28	50.0	413	2	AF1132	D-amino acid dehyd
840	28	50.0	292	2	A60547	hypothetical prote	913	28	50.0	414	2	AB2242	hypothetical prote
841	28	50.0	296	2	C49539	xyloglucan endo-1,	914	28	50.0	415	2	F91209	low affinity trypt
842	28	50.0	297	2	B70894	probable lipu prot	915	28	50.0	415	2	A86056	low affinity trypt
843	28	50.0	299	2	A43953	N-chimerin - commo	916	28	50.0	415	2	A39412	tryptophan transpo
844	28	50.0	299	2	S08242	N-chimerin - human	917	28	50.0	415	2	E83281	precorrin-ty-depen
845	28	50.0	305	1	S52924	coproporphyrinogen	918	28	50.0	417	1	WMBEHA	S2K immediate-earl
846	28	50.0	305	2	H83344	hypothetical prote	919	28	50.0	419	2	T10652	hypothetical prote
847	28	50.0	308	2	AB1957	hypothetical prote	920	28	50.0	420	2	T46460	hypothetical prote
848	28	50.0	308	2	JC2253	chitinase (EC 3.2,	921	28	50.0	421	2	D81374	probable oxidoredu
849	28	50.0	309	2	AG0368	coproporphyrinogen	922	28	50.0	423	2	A33395	acid phosphatase (
850	28	50.0	310	1	Q0BE28	BRRF1 protein - hu	923	28	50.0	425	2	G83969	cell-division prot
851	28	50.0	310	2	T31125	hypothetical prote	924	28	50.0	425	2	AC2756	MFS permease (limp
852	28	50.0	311	2	H82744	methyltransferase	925	28	50.0	426	1	BVECID	lysine 6-monooxyge
853	28	50.0	317	2	A11887	coproporphyrinogen	926	28	50.0	429	2	F72784	probable dihydroor
854	28	50.0	318	2	S14948	chitinase (EC 3.2,	927	28	50.0	429	2	T21113	hypothetical prote
855	28	50.0	319	2	JC2252	chitinase (EC 3.2,	928	28	50.0	432	2	AF0567	probable permease
856	28	50.0	320	2	T30894	lipase homolog TO	929	28	50.0	433	2	B64603	anaerobic glycerol
857	28	50.0	322	2	S54806	chitinase (EC 3.2,	930	28	50.0	433	2	A71912	glycerol-3-phospha
858	28	50.0	322	2	S59953	chitinase (EC 3.2,	931	28	50.0	435	2	H83307	probable porin PA2
859	28	50.0	323	2	T03614	chitinase (EC 3.2,	932	28	50.0	439	2	AF0551	branched chain ami
860	28	50.0	324	2	B25102	reaction center pr	933	28	50.0	439	2	A64769	branched-chain ami
861	28	50.0	327	2	D87645	sensor histidine k	934	28	50.0	439	2	C90685	branched-chain ami
862	28	50.0	328	2	T50104	hypothetical prote	935	28	50.0	439	2	G85535	branched-chain ami
863	28	50.0	330	2	C82184	chitinase (EC 3.2,	936	28	50.0	442	2	QJ0007	branched-chain ami
864	28	50.0	335	2	B45511	chitinase (EC 3.2,	937	28	50.0	442	2	A10121	probable lysine 6-
865	28	50.0	335	2	T44728	probable hydrolase	938	28	50.0	442	2	C82823	type I restriction
866	28	50.0	336	1	S18750	chitinase (EC 3.2,	939	28	50.0	443	2	JC4067	hypothetical 50.1k
867	28	50.0	336	2	D69496	conserved hypotet	940	28	50.0	444	2	C75428	probable permease
868	28	50.0	340	2	S47712	coproporphyrinogen	941	28	50.0	445	2	T44482	lysine 6-monooxyge
869	28	50.0	340	2	S48030	probable chitinase	942	28	50.0	447	2	T22163	hypothetical prote
870	28	50.0	340	2	T14711	probable transposa	943	28	50.0	447	2	T35519	hypothetical prote
871	28	50.0	341	2	B86503	acyltransferase [i	944	28	50.0	452	2	G86170	hypothetical prote
872	28	50.0	342	2	H86007	probable 3' termin	945	28	50.0	454	2	F90875	probable portal pr
873	28	50.0	342	2	T13196	hypothetical prote	946	28	50.0	457	2	B82216	conserved hypotet
874	28	50.0	342	2	S23438	hypothetical prote	947	28	50.0	462	2	E81551	lipid A biosynthes
875	28	50.0	343	2	F91161	RNA 3'-terminal ph	948	28	50.0	462	2	H95914	hypothetical membr
876	28	50.0	344	2	F90500	glycolate oxidase	949	28	50.0	464	2	B64173	hypothetical prote
877	28	50.0	345	2	AB2348	probable ADP-hepto	950	28	50.0	464	2	F96834	probable sulfate t
878	28	50.0	347	2	AB1976	coproporphyrinogen	951	28	50.0	465	2	H84347	glycerol-3-phospha
879	28	50.0	350	2	T29436	hypothetical prote	952	28	50.0	467	2	B72119	acyltransferase -
880	28	50.0	354	2	T14980	probable transposa	953	28	50.0	469	2	G87513	beta-glucosidase [
881	28	50.0	356	2	A25918	thrombomodulin - b	954	28	50.0	470	2	S47892	neutral amino acid
882	28	50.0	362	2	I71998	MHC H-2D-k protein	955	28	50.0	471	2	T49019	probable RNA bindi
883	28	50.0	363	2	T22594	hypothetical prote	956	28	50.0	476	2	B96547	probable protein k
884	28	50.0	364	2	E71433	probable metallopr	957	28	50.0	483	2	AG1898	thioredoxin reduct
885	28	50.0	372	2	C39364	GDP-1 embryonic gr	958	28	50.0	487	2	G71432	hypothetical prote
886	28	50.0	373	2	T40602	hypothetical prote	959	28	50.0	489	2	AG3038	conserved hypotet
887	28	50.0	375	2	F64565	spore coat polysac	960	28	50.0	491	2	G83850	ATP-dependent DNA
888	28	50.0	375	2	A95867	probable pyrroloqu	961	28	50.0	493	2	S71489	sulfinoalanine dec
889	28	50.0	376	1	K1BE17	thymidine kinase (962	28	50.0	496	2	C87194	probable transmem
890	28	50.0	376	1	K1BEK5	thymidine kinase (963	28	50.0	498	2	AC1930	ammonium transport
891	28	50.0	376	1	K1BETC	thymidine kinase (964	28	50.0	498	2	B97537	probable transmem
892	28	50.0	378	2	C71861	probable sugar nuc	965	28	50.0	500	2	T47257	thiamin biosynthes
893	28	50.0	378	2	H96773	hypothetical prote	966	28	50.0	505	2	A24707	cytochrome-c oxida
894	28	50.0	386	2	A12152	hypothetical prote	967	28	50.0	506	2	T41079	probable alpha 1,2
895	28	50.0	387	2	T02780	probable conjugal	968	28	50.0	506	2	T29968	hypothetical prote
896	28	50.0	387	2	B83548	hypothetical prote	969	28	50.0	509	2	C69491	probable acid-CoA
897	28	50.0	388	2	D81882	probable succinate	970	28	50.0	513	2	T37180	probable membrane
898	28	50.0	388	2	F81137	succinyl-CoA synth	971	28	50.0	515	2	D98247	next protein (AF11
899	28	50.0	388	2	JQ0189	oligogalacturonide	972	28	50.0	518	2	T09354	hypothetical prote
900	28	50.0	391	2	S49300	AWJL236 protein -	973	28	50.0	529	2	AH1463	conserved membrane
901	28	50.0	392	2	C83151	probable two-compo	974	28	50.0	532	1	WZBEF5	59K transcription
902	28	50.0	394	2	JC1420	translation elonga	975	28	50.0	536	2	T42606	probable transcrip
903	28	50.0	396	2	A97562	S-adenosylmethioni	976	28	50.0	537	2	B81734	Aas bifunctional p
904	28	50.0	397	2	T71339	urea transport pro	977	28	50.0	537	2	H71471	probable acylglyce
905	28	50.0	401	2	A75388	NADH dehydrogenase	978	28	50.0	537	2	T48599	hypothetical prote

acetyl-CoA C-acetyl
beta ketoacyl-acyl
aminotransferase,
pantothenate metab
hypothetical prote
D-alanine dehydrog
D-amino acid dehyd
hypothetical prote
low affinity trypt
low affinity trypt
tryptophan transpo
precorrin-ty-depen
S2K immediate-earl
hypothetical prote
hypothetical prote
probable oxidoredu
acid phosphatase (

979 28 50.0 538 2 E72752
 980 28 50.0 544 2 I55454
 981 28 50.0 548 2 A75357
 982 28 50.0 554 2 D72760
 983 28 50.0 559 2 S54358
 984 28 50.0 559 2 A46311
 985 28 50.0 565 2 G98813
 986 28 50.0 567 2 A86262
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 992 28 50.0 594 2 T06369
 993 28 50.0 599 2 T15552
 994 28 50.0 615 2 S77332
 995 28 50.0 615 2 T34392
 996 28 50.0 616 2 S33908
 997 28 50.0 620 1 W2BEC1
 998 28 50.0 622 2 B96751
 999 28 50.0 629 2 E47096
 1000 28 50.0 630 2 G87753

hypothetical prote
 neuroglycan C prec
 hypothetical prote
 hypothetical prote
 transcription fact
 pol polypeptin
 DNA polymerase III
 hypothetical prote
 hypothetical prote
 phosphoprotein pho
 hypothetical prote
 conserved hypothet
 NADH2 dehydrogenas
 probable 3,4-dihyd
 hypothetical prote
 NADH2 dehydrogenas
 hypothetical prote
 glucan 1,4-alpha-g
 gene 28 protein -
 hypothetical prote
 membrane transloca
 protein C43E11.8 [

ALIGNMENTS

RESULT 1
 YXMST
 thymidylate synthase (EC 2.1.1.45) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
 C:Accession: A26323; A24157; I48858
 R:Deng, T.; Li, D.; Jeng, C.H.; Johnson, L.F.
 J. Biol. Chem. 261, 16000-16005, 1986
 A>Title: Structure of the gene for mouse thymidylate synthase. Locations of introns and
 A:Reference number: A26323; MUID:87057259; PMID:3782103
 A:Accession: A26323
 A:Molecule type: DNA
 A:Residues: 1-307 <DEN>
 R:Perryman, S.M.; Rosana, C.; Deng, T.; Vanin, E.F.; Johnson, L.F.
 Mol. Biol. Evol. 3, 313-321, 1986
 A>Title: Sequence of a cDNA for mouse thymidylate synthase reveals striking similarity w
 A:Reference number: A24157; MUID:88174353; PMID:3444407
 A:Accession: A24157
 A:Molecule type: mRNA
 A:Residues: 1-307 <PER>
 R:Deng, T.L.; Li, Y.; Johnson, L.F.
 Nucleic Acids Res. 17, 645-658, 1989
 A>Title: Thymidylate synthase gene expression is stimulated by some (but not all) intron
 A:Reference number: I48858; MUID:89128436; PMID:2915925
 A:Accession: I48858
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 236-265 <RES>
 R:Genetics:
 C:Introns: 63/1; 87/3; 146/1; 180/1; 238/3; 262/3
 C:Superfamily: thymidylate synthase; thymidylate synthase homology
 C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F:24-307/Domain: thymidylate synthase homology <TDS>
 F:193/Active site: Cys #status predicted

Query Match 100.0%; Score 56; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
 |||||
 Db 183 LMALPPCHAL 192

RESULT 2

SS3715

thymidylate synthase (EC 2.1.1.45) - rat
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S53715

R:Ciesla, J.; Weiner, K.X.B.; Weiner, R.S.; Reston, J.T.; Maley, G.F.; Maley, F.
 Biochim. Biophys. Acta 1261, 233-242, 1995

A>Title: Isolation and expression of rat thymidylate synthase cDNA: phylogenetic compari
 A:Reference number: S53715; MUID:95226450; PMID:7711067

A:Accession: S53715

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-307 <CIE>

A:Cross-references: UNIPROT:P45352; UNIPARC:UPI0000112C76; EMBL:L12138; NID:g207327; PID
 C:Superfamily: thymidylate synthase; thymidylate synthase homology

C:Keywords: methyltransferase

F:24-307/Domain: thymidylate synthase homology <TDS>

Query Match 100.0%; Score 56; DB 2; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10

|||||

Db 183 LMALPPCHAL 192

RESULT 3

YXHUT

thymidylate synthase (EC 2.1.1.45) - human

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
 C:Accession: A23047; I55318; J00120; A22393; A33842

R:Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.

Nucleic Acids Res. 13, 2035-2043, 1985

A>Title: Nucleotide sequence of a functional cDNA for human thymidylate synthase.
 A:Reference number: A23047; MUID:85215597; PMID:2987839

A:Accession: A23047

A:Molecule type: mRNA

A:Residues: 1-313 <TKA>

A:Cross-references: UNIPROT:P04818; UNIPARC:UPI0000001225; EMBL:X02308; NID:g37478; PIDN
 R:Kaneda, S.; Nalbantoglu, J.; Takeishi, K.; Shimizu, K.; Gotoh, O.; Seno, T.; Ayusawa,

J. Biol. Chem. 265, 20277-20284, 1990

A>Title: Structural and Functional Analysis of the Human Thymidylate Synthase Gene.
 A:Reference number: I55318; MUID:910556070; PMID:2243092

A:Accession: I55318

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <RES>

A:Cross-references: UNIPARC:UPI0000001225; GB:D00596; NID:g220135; PIDN:BAA00472.1; PID:
 R:Takeishi, K.; Kaneda, S.; Ayusawa, D.; Shimizu, K.; Gotoh, O.; Seno, T.

J. Biochem. 106, 575-583, 1989

A>Title: Human thymidylate synthase gene: isolation of phage clones which cover a functi
 A:Reference number: J00120; MUID:90110051; PMID:2532645

A:Accession: J00120

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-68 <TA2>

A:Cross-references: UNIPARC:UPI000016B136; GB:D00517; NID:g220133; PIDN:BAA00404.1; PID:
 R:Shimizu, K.; Ayusawa, D.; Takeishi, K.; Seno, T.

J. Biochem. 97, 845-850, 1985

A>Title: Purification and NH2-terminal amino acid sequence of human thymidylate synthase
 A:Reference number: A22393; MUID:85261174; PMID:3839505

A:Accession: A22393

A:Molecule type: protein

A:Residues: 2-25 <SHI>

A:Cross-references: UNIPARC:UPI00001722FE

R:Davidson, V.J.; Sitawaraporn, W.; Santl, D.V.

J. Biol. Chem. 264, 9145-9148, 1989

A>Title: Expression of human thymidylate synthase in Escherichia coli.

A:Reference number: A33842; MUID:89255401; PMID:2656695

A:Accession: A33842
 A:Molecule type: protein
 A:Residues: 2-10 <DAV>
 A:Cross-references: UNIPARC:UPI00001722FP
 C:Genetics:
 A:Gene: GDB:TYMS
 A:Cross-references: GDB:120465; OMIM:188350
 A:Map position: 18p11.32-18p11.32
 A:Introns: 69/1; 93/3; 152/1; 186/1; 244/3; 268/3
 C:Superfamily: thymidylate synthase; thymidylate synthase homology
 C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F:30-313/Domain: thymidylate synthase homology <YDS>
 F:199/Active site: Cys #status predicted

Query Match 100.0%; Score 56; DB 1; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 LMALPPCHAL 10
 |||||
 DB 189 LMALPPCHAL 198

RESULT 4
 GB1050
 thymidylate synthase NM1709 [imported] - Neisseria meningitidis (strain MC58 serogroup C)
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: GB1050
 R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vitti, A.
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: AB1000; MUID:20175755; PMID:10710307
 A:Accession: GB1050
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <TET>
 A:Cross-references: UNIPROT:Q9JY72; UNIPARC:UPI00001378E6; GB:AE002098; NID
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NM1709
 C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 92.9%; Score 52; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHAL 149

RESULT 5
 AB1825
 thymidylate synthase (EC 2.1.1.45) NMA1963 [imported] - Neisseria meningitidis (strain Z)
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
 C:Accession: AB1825
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, P.; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, N.
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: AB1775; MUID:20222556; PMID:10761919
 A:Accession: AB1825
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <PAR>
 A:Cross-references: UNIPROT:Q9JY75; UNIPARC:UPI00001378E5; GB:AL162757; GB:AL157959; NID
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:

A:Gene: thyA; NMA1963
 C:Superfamily: thymidylate synthase; thymidylate synthase homology
 C:Keywords: methyltransferase

Query Match 92.9%; Score 52; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHAL 149

RESULT 6

DB3602
 thymidylate synthase PA0342 [imported] - Pseudomonas aeruginosa (strain PAO1)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
 C:Accession: DB3602
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brinkman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
 A:Reference number: AB2950; MUID:20437337; PMID:10984043
 A:Accession: DB3602
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <STO>
 A:Cross-references: UNIPROT:Q916P1; UNIPARC:UPI00001378E8; GB:AE004472; GB:AE004091; NID
 A:Experimental source: strain PAO1
 C:Genetics:
 A:Gene: thyA; PA0342
 C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 92.9%; Score 52; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.077;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHAL 149

RESULT 7

AB1309
 thymidylate synthase homolog lmo1874 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AB1309
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AB1309
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-314 <GLA>
 A:Cross-references: UNIPROT:O8Y626; UNIPARC:UPI00000550D5; GB:NC_003210; PIDN:CAC99952.1
 A:Experimental source: strain EGD-e
 C:Genetics:

A:Gene: lmo1874
 C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 87.5%; Score 49; DB 2; Length 314;
 Best Local Similarity 88.9%; Pred. No. 0.3;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10

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Db      191 MALPPCHSL 199
|||||||:|

RESULT 8
AB1681
thymidylate synthase homolog lin1988 [imported] - Listeria innocua (strain Clp11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB1681
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefetz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1681
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <GLA>
A;Cross-references: UNIPROT:Q92AD4; UNIPARC:UPI00001378D6; GB:AL592022; PIDN:CAC97218.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin1988
C;Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match      87.5%; Score 49; DB 2; Length 314;
Best Local Similarity 88.9%; Pred. No. 0.3;
Matches      8; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

Oy      2 MALPPCHAL 10
|||||||:|
Db      191 MALPPCHSL 199

RESULT 9
C70881
probable thvA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004
C;Accession: C70881
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70881
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-263 <COL>
A;Cross-references: UNIPROT:Q33306; UNIPARC:UPI00001378E3; GB:AL008967; GB:AL123456; NID
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: thvA
C;Superfamily: thymidylate synthase; thymidylate synthase homology
F;1-263/Domain: thymidylate synthase homology <TDS>

Query Match      85.7%; Score 48; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Oy      2 MALPPCHA 9
|||||||
Db      141 MALPPCHA 148

RESULT 10
S35239
thymidylate synthase (EC 2.1.1.45) B - Bacillus subtilis (strain ATCC 6633)

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C;Species: Bacillus subtilis
C;Date: 03-Feb-1994 #sequence_revision 02-Jul-1998 #text_change 05-Oct-2004
C;Accession: S35239
R;Montorsi, M.; Lorenzetti, R.
Mol. Gen. Genet. 239, 1-5, 1993
A;Title: Heat-stable and heat-labile thymidylate synthases B of Bacillus subtilis: compa
A;Reference number: S35239; MUID:93287974; PMID:8510640
A;Accession: S35239
A;Molecule type: DNA
A;Residues: 1-264 <MON>
A;Cross-references: UNIPROT:P11044; UNIPARC:UPI000016B9B7; EMBL:X69661; NID:G311939; PID
C;Comment: In this strain, unlike strain 168 (see PIR:SYB5TB), thymidylate synthase B is
C;Genetics:
A;Gene: thvB
C;Function:
A;Description: catalyzes the methylation of dUMP to dTMP by 5,10-methylenetetrahydrofolat
A;Pathway: deoxyribonucleotide biosynthesis
C;Superfamily: thymidylate synthase; thymidylate synthase homology
C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F;1-264/Domain: thymidylate synthase homology <TDS>
F;146/Active site: Cys #status predicted

```

```

Query Match      85.7%; Score 48; DB 1; Length 264;
Best Local Similarity 88.9%; Pred. No. 0.39;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

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Oy      2 MALPPCHAL 10
|||||||
Db      141 MALPPCHCL 149

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RESULT 11

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AI2827
thymidylate synthase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
C;Accession: AI2827
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2827
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <KUR>
A;Cross-references: UNIPROT:Q8UDS3; UNIPARC:UPI00001378C3; GB:AE008688; PIDN:AAL43039.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: thvA
A;Map position: circular chromosome
C;Superfamily: thymidylate synthase; thymidylate synthase homology

```

```

Query Match      85.7%; Score 48; DB 2; Length 264;
Best Local Similarity 88.9%; Pred. No. 0.39;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

```

```

Oy      2 MALPPCHAL 10
|||||||
Db      141 MALPPCHCL 149

```

RESULT 12

```

AB3328
thymidylate synthase (EC 2.1.1.45) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004
C;Accession: AB3328
R;DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee

```

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3328
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <KUR>
A:Cross-references: UNIPROT:Q8YI37; UNIPARC:UPI0000057D4A; GB:AE008917; PIDN:AAL51789.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0608
A:Map position: 1
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: methyltransferase

Query Match 85.7%; Score 48; DB 2; Length 264;
Best Local Similarity 88.9%; Pred. No. 0.39; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 2 MALPPCHAL 10
|||
Db 141 MALPPCHCL 149

RESULT 13
A87099
thymidylate synthase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C:Accession: A87099
R:Colo, S.T.; Rigmiller, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; PMID:21128732; PMID:11234002
A:Accession: A87099
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <STO>
A:Cross-references: UNIPROT:Q9CBW0; UNIPARC:UPI00001378E0; GB:AL450380; NID:gl3093353; F
C:Genetics:
A:Gene: thyA
C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 85.7%; Score 48; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.39; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

QY 2 MALPPCHA 9
|||
Db 144 MALPPCHA 151

RESULT 14
G97605
hypothetical protein AGR_C_3709 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97605
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: G97605
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <KUR>
A:Cross-references: UNIPARC:UPI00001643B8; GB:AE007869; PIDN:AAK87800.1; PID:gl5151714;
C:Genetics:
A:Gene: AGR_C_3709

A:Map position: circular chromosome
C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 85.7%; Score 48; DB 2; Length 279;
Best Local Similarity 88.9%; Pred. No. 0.41; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 2 MALPPCHAL 10
|||
Db 156 MALPPCHCL 164

RESULT 15
CB87512
thymidylate synthase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C:Accession: CB87512
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; PMID:21173698; PMID:11259647
A:Accession: CB87512
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-279 <STO>
A:Cross-references: UNIPROT:Q9A6H0; UNIPARC:UPI00001378CA; GB:AE005673; NID:gl3423613; I
C:Genetics:
A:Gene: CC2124
C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 85.7%; Score 48; DB 2; Length 279;
Best Local Similarity 88.9%; Pred. No. 0.41; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 2 MALPPCHAL 10
|||
Db 157 MALPPCHCL 165

RESULT 16
SYBEAT
thymidylate synthase (EC 2.1.1.45) - ateline herpesvirus 2 (strain 810)
C:Species: ateline herpesvirus 2
A:Note: host Ateles spp. (spider monkey)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 05-Oct-2004
C:Accession: A28879
R:Richter, J.; Puchtler, I.; Fleckenstein, B.
J. Virol. 62, 3530-3535, 1988
A:Title: Thymidylate synthase gene of herpesvirus ateles.
A:Reference number: A28879; PMID:88300915; PMID:3404583
A:Accession: A28879
A:Molecule type: DNA
A:Residues: 1-230 <RIC>
A:Cross-references: UNIPROT:P12462; UNIPARC:UPI00001378D1; GB:M22036; NID:g331063; PIDN
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F:7-290/Domain: thymidylate synthase homology <TDS>
F:172/Active site: Cys #status predicted

Query Match 85.7%; Score 48; DB 1; Length 290;
Best Local Similarity 88.9%; Pred. No. 0.42; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0

QY 2 MALPPCHAL 10
|||
Db 167 MALPPCHVL 175

RESULT 17
T42984
thymidylate synthase; thymidylate synthase homology

thymidylate synthase (EC 2.1.1.45) - ateline herpesvirus 3 (strain 73)
C:Species: ateline herpesvirus 3
A:Variety: strain 73
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42984
R:Albrecht, J.C.; Fleckenstein, B.
Submitted to the EMBL Data Library, August 1998
A:Description: Primary structure of the herpesvirus ateles genome.
A:Reference number: Z22274
A:Accession: T42984
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <ALB>
A:Cross-references: UNIPROT:Q9Y7J6; UNIPARC:UPI0000F8B14; EMBL:AF083424; PIDN:AAC95595.
A:Experimental source: strain 73
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: methyltransferase

Query Match 85.7%; Score 48; DB 2; Length 290;
Best Local Similarity 88.9%; Pred. No. 0.42;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 167 MALPPCHVL 175
|||||

RESULT 18
SVBE13
thymidylate synthase (EC 2.1.1.45) - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Oct-2004
C:Accession: D27342
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657; PMID:3018124
A:Accession: D27342
A:Molecule type: DNA
A:Residues: 1-301 <DAV>
A:Cross-references: UNIPROT:P09249; UNIPARC:UPI00001378F0; EMBL:X04370; NID:G59989; PIDN:
C:Genetics:
A:Gene: 13
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F:18-301/Domain: thymidylate synthase homology <TDS>
F:183/Active site: Cys #status predicted

Query Match 85.7%; Score 48; DB 1; Length 301;
Best Local Similarity 80.0%; Pred. No. 0.44;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 177 LMALPPCHTL 186
|||||

RESULT 19
SVLBT
thymidylate synthase (EC 2.1.1.45) - Lactobacillus casei
C:Species: Lactobacillus casei
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 05-Oct-2004
C:Accession: A29817; A00548
R:Painter, K.; Davisson, V.J.; Santi, D.V.
DNA 7, 235-241, 1988
A:Title: Cloning, sequencing, and expression of the Lactobacillus casei thymidylate synth
A:Reference number: A29817; MUID:88283342; PMID:2840247
A:Accession: A29817
A:Molecule type: DNA
A:Residues: 1-316 <PIN>
A:Cross-references: UNIPROT:P00469; UNIPARC:UPI00001123C7; GB:M19653
R:Malay, G.F.; Bellisario, R.L.; Guarino, D.U.; Maley, F.
J. Biol. Chem. 254, 1301-1304, 1979

A:Title: The primary structure of Lactobacillus casei thymidylate synthetase. III. The
te amino acid sequence of the enzyme.
A:Reference number: A00548; MUID:79109713; PMID:105005
A:Accession: A00548
A:Molecule type: protein
A:Residues: 1-316 <MAL>
A:Cross-references: UNIPARC:UPI00001123C7
A:Note: this is the final paper of a series
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; homodimer; methyltransferase
F:3-316/Domain: thymidylate synthase homology <TDS>
F:198/Active site: Cys #status experimental

Query Match 85.7%; Score 48; DB 1; Length 316;
Best Local Similarity 88.9%; Pred. No. 0.46;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 193 MALPPCHTL 201
|||||

RESULT 20
T05277
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Arabidopsis
N:Alternate names: protein T4L20.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T05277
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyssehaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
Submitted to the Protein Sequence Database, September 1998
A:Reference number: Z15406
A:Accession: T05277
A:Molecule type: DNA
A:Residues: 1-518 <BEV>
A:Cross-references: UNIPROT:Q05763; UNIPARC:UPI000000BF1C; EMBL:AL023094
A:Experimental source: cultivar Columbia; BAC clone T4L20
C:Genetics:
A:Map position: 4
A:Introns: 138/2; 267/3; 282/3; 304/3; 325/2; 350/2; 447/1; 482/3
A:Note: T4L20.150
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: methyltransferase; NADP; oxidoreductase
F:18-141/Domain: type I dihydrofolate reductase homology <DFR>
F:235-518/Domain: thymidylate synthase homology <TDS>

Query Match 85.7%; Score 48; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8
DB 394 LMALPPCH 401
|||||

RESULT 21
E84539
dihydrofolate reductase-thymidylate synthase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: E84539
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-519 <STO>
A:Cross-references: UNIPROT:Q05762; UNIPARC:UPI00000017CC; GB:AE002093; NID:G4544392; PI

C:Genetics:

A:Gene: At2g16370
A:Map position: 2
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy

Query Match 85.7%; Score 48; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

|||||

Db 395 LMALPPCH 402

RESULT 22

S35272 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - carrot

C:Species: Daucus carota (carrot)
C:Date: 10-Dec-1993 #sequence_revision 19-Jan-1996 #text_change 31-Dec-2004
C:Accession: S35272; S32242

R:Luco, M.; Piffanelli, P.; Rastelli, L.; Cella, R.

Plant Mol. Biol. 22, 427-435, 1993

A:Title: Molecular cloning and analysis of a cDNA coding for the bifunctional dihydrofol
A:Reference number: S35272; MUID:93320381; PMID:8329682

A:Accession: S35272

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-528 <LUO>

A:Cross-references: UNIPROT:P45350; UNIPARC:UPI00001298A3; EMBL:Z17306; NID:G288614; PID
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy

C:Keywords: methyltransferase; NADP; oxidoreductase

F:23-146/Domain: type I dihydrofolate reductase homology <DPR>

F:244-528/Domain: thymidylate synthase homology <TDS>

Query Match 85.7%; Score 48; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 0.74;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

|||||

Db 403 LMALPPCH 410

RESULT 23

S55683

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - soybean

C:Species: Glycine max (soybean)
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 31-Dec-2004
C:Accession: S55683

R:Wang, M.; Ratnam, S.; Freisheim, J.H.

Biochim. Biophys. Acta 1261, 325-336, 1995

A:Title: Cloning, nucleotide sequence and expression of the bifunctional dihydrofolate r
A:Reference number: S55683; MUID:95260857; PMID:7742362

A:Accession: S55683

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-530 <WAN>

A:Cross-references: UNIPROT:P51820; UNIPARC:UPI00001298AD; GB:S78087; NID:G999189; PIDN:
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy

C:Keywords: methyltransferase; NADP; oxidoreductase

F:26-149/Domain: type I dihydrofolate reductase homology <DPR>

F:247-530/Domain: thymidylate synthase homology <TDS>

Query Match 85.7%; Score 48; DB 2; Length 530;

Best Local Similarity 100.0%; Pred. No. 0.74;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

|||||

Db 406 LMALPPCH 413

RESULT 24

T14315

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - carrot
N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)
C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004

C:Accession: T14315; S49321

R:Luco, M.; Piffanelli, P.; Rastelli, L.; Cella, R.

Plant Mol. Biol. 22, 427-435, 1993

A:Title: Molecular cloning and analysis of a cDNA coding for the bifunctional dihydrofol
A:Reference number: S35272; MUID:93320381; PMID:8329682

A:Accession: T14315

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-577 <LUO>

A:Cross-references: UNIPROT:Q39687; UNIPARC:UPI00000A1A8D; EMBL:AJ003139; NID:G3097055;
R:Luco, M.; Orsi, R.; Cella, R.

submitted to the EMBL Data Library, May 1994

A:Description: Plastidial localization of the bifunctional dihydrofolate reductase-thymi
A:Reference number: S49321

A:Accession: S49321

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-49 <LU2>

A:Cross-references: UNIPARC:UPI000016DD5B; EMBL:Z33383; NID:G5566699; PID:G556700

C:Genetics:

A:Introns: 24/3; 192/2; 325/3; 340/3; 362/3; 383/2; 408/2; 463/3; 505/1; 541/3

A>Note: DHFR-TS

C:Function:

A:Description: bifunctional enzyme catalyzes the reduction of folate into tetrahydrofola
rt of the enzyme

A>Note: bifunctional enzyme in plants and protozoan

C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: methyltransferase; multifunctional enzyme; NADP; oxidoreductase

F:72-195/Domain: type I dihydrofolate reductase homology <DPR>

F:293-577/Domain: thymidylate synthase homology <TDS>

Query Match 85.7%; Score 48; DB 2; Length 577;

Best Local Similarity 100.0%; Pred. No. 0.81;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

|||||

Db 452 LMALPPCH 459

RESULT 25

S55667

thymidylate synthase 70 - equine herpesvirus 2

C:Species: equine herpesvirus 2

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S55667

R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A:Title: The DNA sequence of equine herpesvirus 2.

A:Reference number: S55594; MUID:95302501; PMID:7783207

A:Accession: S55667

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-289 <TEL>

A:Cross-references: UNIPROT:Q89940; UNIPARC:UPI00001378D2; GB:U20824; NID:G695172; PIDN:
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

C:Superfamily: thymidylate synthase; thymidylate synthase homology

F:6-289/Domain: thymidylate synthase homology <TDS>

Query Match 83.9%; Score 47; DB 2; Length 289;

Best Local Similarity 88.9%; Pred. No. 0.63;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10

|||||

Db 166 MALPPCHLL 174

```
RESULT 26
E75250
thymidylate synthase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C:Accession: E75250
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75250
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <WHI>
A:Cross-references: UNIPROT:Q9RB67; UNIPARC:UPI00000D3FP9; GB:AE002092; GB:AE000513; NID
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2630
A:Map position: 1
C:Superfamily: thymidylate synthase

Query Match 83.9%; Score 47; DB 2; Length 387;
Best Local Similarity 88.9%; Pred. No. 0.83;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 264 MALPPCHLL 272

RESULT 27
RDINTZ
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m
N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)
C:Species: Leishmania major
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 31-Dec-2004
C:Accession: A23403; A24311; A24734; S08691; S14709
R:Beverley, S.M.; Ellenberger, T.E.; Cordingley, J.S.
Proc. Natl. Acad. Sci. U.S.A. 83, 2584-2588, 1986
A:Title: Primary structure of the gene encoding the bifunctional dihydrofolate reductase
A:Reference number: A23403; MUID:86205996; PMID:3458220
A:Accession: A23403
A:Molecule type: DNA
A:Residues: 1-520 <BEV>
A:Cross-references: UNIPROT:P07382; UNIPARC:UPI00001298A5; EMBL:M12734; NID:G159309; PID
R:Grumont, R.; Washtien, W.L.; Caput, D.; Santi, D.V.
Proc. Natl. Acad. Sci. U.S.A. 83, 5387-5391, 1986
A:Title: Bifunctional thymidylate synthase-dihydrofolate reductase from Leishmania tropi
A:Reference number: A24311; MUID:86287263; PMID:3461439
A:Accession: A24311
A:Molecule type: DNA
A:Residues: 1-48, 'S', 50-71, 'BEAQR', 77-124, 'RML', 128-306, 'T', 308-396, 'V', 398-520 <GRU>
A:Cross-references: UNIPARC:UPI0000172305; GB:M14330
R:Garvey, E.P.; Santi, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 7188-7192, 1985
A:Title: Limited proteolysis of the bifunctional thymidylate synthase-dihydrofolate red
A:Reference number: A24734; MUID:86042631; PMID:3903747
A:Accession: A24734
A:Molecule type: Protein
A:Residues: 334-345, 'G', 347, 349-352, 354-358, 360-361 <GAR>
A:Cross-references: UNIPARC:UPI0000172306
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:26-166/Domain: type I dihydrofolate reductase homology <DFR>
F:234-520/Domain: thymidylate synthase homology <TDS>
F:400/Active site: Cys #status predicted

Query Match 83.9%; Score 47; DB 1; Length 520;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 264 MALPPCHLL 272

RESULT 28
RDINTZ
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m
N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)
C:Species: Leishmania mexicana amazonensis
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: S15756; S08660
R:Nelson, K.; Alonso, G.; Langer, P.J.; Beverley, S.M.
Nucleic Acids Res. 18, 2819, 1990
A:Title: Sequence of the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene of
A:Reference number: S15756; MUID:90251468; PMID:2339068
A:Accession: S15756
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-520 <NEL>
A:Cross-references: UNIPROT:P16126; UNIPARC:UPI00001298A4; EMBL:X51735; NID:G9470; PIDN:
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:26-166/Domain: type I dihydrofolate reductase homology <DFR>
F:234-520/Domain: thymidylate synthase homology <TDS>
F:400/Active site: Cys #status predicted

Query Match 83.9%; Score 47; DB 1; Length 520;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 395 MALPPCHLL 403

RESULT 29
RDZQTB
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium c
C:Species: Plasmodium chabaudi
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: A33484
R:Coman, A.F.; Lew, A.M.
Mol. Cell. Biol. 9, 5182-5188, 1989
A:Title: Antifolate drug selection results in duplication and rearrangement of chromosom
A:Reference number: A33484; MUID:90097935; PMID:2601715
A:Accession: A33484
A:Molecule type: DNA
A:Residues: 1-583 <COM>
A:Cross-references: UNIPROT:P20712; UNIPARC:UPI00001298A9; GB:M30834; NID:G160265; PIDN:
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:24-164/Domain: type I dihydrofolate reductase homology <DFR>
F:300-583/Domain: thymidylate synthase homology <TDS>
F:465/Active site: Cys #status predicted

Query Match 83.9%; Score 47; DB 1; Length 583;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 460 MALPPCHLL 468

RESULT 30
RDZQK1
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - malaria para
C:Species: Plasmodium falciparum
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: A39975; B31262; B31262; G31262; C31262; E31262; F31262; J30208; D31262
R:Bzik, D.J.; Li, W.; Horii, T.; Inselburg, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 8360-8364, 1987
```

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QY 2 MALPPCHAL 10
|||||||
DB 395 MALPPCHLL 403

RESULT 28
RDINTZ
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Leishmania m
N:Contains: dihydrofolate reductase (EC 1.5.1.3); thymidylate synthase (EC 2.1.1.45)
C:Species: Leishmania mexicana amazonensis
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: S15756; S08660
R:Nelson, K.; Alonso, G.; Langer, P.J.; Beverley, S.M.
Nucleic Acids Res. 18, 2819, 1990
A:Title: Sequence of the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene of
A:Reference number: S15756; MUID:90251468; PMID:2339068
A:Accession: S15756
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-520 <NEL>
A:Cross-references: UNIPROT:P16126; UNIPARC:UPI00001298A4; EMBL:X51735; NID:G9470; PIDN:
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:26-166/Domain: type I dihydrofolate reductase homology <DFR>
F:234-520/Domain: thymidylate synthase homology <TDS>
F:400/Active site: Cys #status predicted

Query Match 83.9%; Score 47; DB 1; Length 520;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 395 MALPPCHLL 403

RESULT 29
RDZQTB
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium c
C:Species: Plasmodium chabaudi
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: A33484
R:Coman, A.F.; Lew, A.M.
Mol. Cell. Biol. 9, 5182-5188, 1989
A:Title: Antifolate drug selection results in duplication and rearrangement of chromosom
A:Reference number: A33484; MUID:90097935; PMID:2601715
A:Accession: A33484
A:Molecule type: DNA
A:Residues: 1-583 <COM>
A:Cross-references: UNIPROT:P20712; UNIPARC:UPI00001298A9; GB:M30834; NID:G160265; PIDN:
C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase; multifunctional enzyme;
F:24-164/Domain: type I dihydrofolate reductase homology <DFR>
F:300-583/Domain: thymidylate synthase homology <TDS>
F:465/Active site: Cys #status predicted

Query Match 83.9%; Score 47; DB 1; Length 583;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||||
DB 460 MALPPCHLL 468

RESULT 30
RDZQK1
thymidylate synthase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - malaria para
C:Species: Plasmodium falciparum
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2004
C:Accession: A39975; B31262; B31262; G31262; C31262; E31262; F31262; J30208; D31262
R:Bzik, D.J.; Li, W.; Horii, T.; Inselburg, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 8360-8364, 1987
```


A;Reference number: A46005; MUID:93203215; PMID:8454599
A;Accession: A46005
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-610 <ROO>
A;Cross-references: UNIPROT:Q07422; UNIPARC:UPI00001298AB; GB:L08489; NID:G495706; PIDN
A;Note: sequence extracted from NCBI backbone (NCBIN:127922, NCBIP:127924)
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C;Keywords: methyltransferase; NADP; oxidoreductase
F;4-161/Domain: type I dihydrofolate reductase homology <DPR>
F;324-610/Domain: thymidylate synthase homology <TDS>

Query Match 83.9%; Score 47; DB 2; Length 610;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
||| ||| |||
Db 484 MALPPCHLL 492

RESULT 32
JC6568
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium
C;Species: Plasmodium vivax
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 31-Dec-2004
C;Accession: JC6568
R;de Pecoulas, P.E.; Basco, L.K.; Tahar, R.; Ouatas, T.; Mazabraud, A.
Gene 211, 177-185, 1998
A;Title: Analysis of the Plasmodium vivax dihydrofolate reductase-thymidylate synthase
A;Reference number: JC6568; MUID:98241515; PMID:9573357
A;Accession: JC6568
A;Molecule type: DNA
A;Residues: 1-623 <DPR>
A;Cross-references: UNIPROT:O02604; UNIPARC:UPI00001298AB; EMBL:X98123
C;Genetics:
A;Gene: dhfr-ts
C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy
C;Keywords: methyltransferase; NADP; oxidoreductase
F;340-623/Domain: thymidylate synthase homology <TDS>

Query Match 83.9%; Score 47; DB 2; Length 623;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
||| ||| |||
Db 500 MALPPCHIL 508

RESULT 33
YXSAT3
thymidylate synthase (EC 2.1.1.45) - Staphylococcus aureus plasmid pSK1 transposon Tn40C
C;Species: Staphylococcus aureus
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
C;Accession: S04163; S14178
R;Rouch, D.A.; Messerotti, L.J.; Loo, L.S.L.; Jackson, C.A.; Skurray, R.A.
Mol. Microbiol. 3, 161-175, 1989
A;Title: Trimethoprim resistance transposon Tn4003 from Staphylococcus aureus encodes gr
A;Reference number: S04162; MUID:89343620; PMID:2548057
A;Accession: S04163
A;Molecule type: DNA
A;Residues: 1-318 <ROU>
A;Cross-references: UNIPROT:PI3954; UNIPARC:UPI000000016F; EMBL:X13290; NID:G46747; PIDN
R;Burdeska, A.; Ott, M.; Bannwarth, W.; Then, R.L.
FEBS Lett. 266, 159-162, 1990
A;Title: Identical genes for trimethoprim-resistant dihydrofolate reductase from Staphyl
A;Reference number: S10715; MUID:90306343; PMID:2365064
A;Accession: S14178
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 253-318 <BUR>
A;Cross-references: UNIPARC:UPI0000170002; EMBL:Y07536; NID:G46551; PIDN:CAA68823.1; PI

C:Genetics:

A:Gene: thvA
 A:Genome: plasmid
 C:Superfamily: thymidylate synthase; thymidylate synthase homology
 C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F:6-318/Domain: thymidylate synthase homology <TDS>
 F:201/Active site: Cys #status predicted

Query Match 82.1%; Score 46; DB 1; Length 318;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 196 MALPPCHTM 204

RESULT 34

C89920

thymidylate synthase [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C:Accession: C89920
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89920

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-318 <KUR>

A:Cross-references: UNIPROT:Q99U61; UNIPARC:UPI00001378EE; GB:BA0000018; PID:g13701225; E

A:Experimental source: strain N315

C:Genetics:

A:Gene: thvA

C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 82.1%; Score 46; DB 2; Length 318;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 196 MALPPCHTM 204

RESULT 35

S65570

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Paramecium b

C:Species: Paramecium tetraurelia

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004

C:Accession: S65570
 R:Schlichterle, I.M.; Roos, D.S.; van Houten, J.L.
 Mol. Gen. Genet. 250, 665-673, 1996

A:Title: Cloning and molecular analysis of the bifunctional dihydrofolate reductase-thym

A:Reference number: S65570; MUID:96204506; PMID:8628226

A:Accession: S65570

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-462 <SCH>

A:Cross-references: UNIPROT:Q27828; UNIPARC:UPI00001298A7; EMBL:U03885; NID:g434591; PID

C:Genetics:

A:Genetic code: SGCS

C:Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy

C:Keywords: methyltransferase; NADP; oxidoreductase

F:6-111/Domain: type I dihydrofolate reductase homology <DPR>

F:180-462/Domain: thymidylate synthase homology <TDS>

Query Match 82.1%; Score 46; DB 2; Length 462;
 Best Local Similarity 77.8%; Pred. No. 1.5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10

Db 340 MALPPCHVM 348

RESULT 36

T09609

uroplakin II - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09609

R:Smith, B.A.; Lobban, E.D.; Hall, G.D.; Harnden, P.; Roberts, P.; Selby, P.J.; Trejdos

Am. J. Pathol. 153, 1957-1967, 1998

A:Title: Uroplakin gene expression by normal and neoplastic human urothelium.

A:Reference number: Z16771; MUID:99061442; PMID:9846985

A:Accession: T09609

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-184 <SMI>

A:Cross-references: UNIPROT:O00526; UNIPARC:UPI0000137CD3; EMBL:Y13645; NID:g3483010; PI

A:Experimental source: ureter

Query Match 78.6%; Score 44; DB 2; Length 184;
 Best Local Similarity 87.5%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8

Db 45 LVALPPCH 52

RESULT 37

A54135

uroplakin II precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004

C:Accession: A55603; A54135

R:Lin, J.H.; Zhao, H.; Sun, T.T.

Proc. Natl. Acad. Sci. U.S.A. 92, 679-683, 1995

A:Title: A tissue-specific promoter that can drive a foreign gene to express in the sup

A:Reference number: A55603; MUID:95148601; PMID:7846036

A:Accession: A55603

A:Molecule type: DNA

A:Residues: 1-184 <LIN>

A:Cross-references: UNIPROT:P38575; UNIPARC:UPI00000299F3; GB:U14421; NID:g540198; PIDN:

R:Wu, X.R.; Lin, J.H.; Walz, T.; Haener, M.; Yu, J.; Aebi, U.; Sun, T.T.

J. Biol. Chem. 269, 13716-13724, 1994

A:Title: Mammalian uroplakins. A group of highly conserved urothelial differentiation-re

A:Reference number: A54135; MUID:94230489; PMID:8175808

A:Accession: A54135

A:Molecule type: mRNA

A:Residues: 1-184 <WUA>

A:Cross-references: UNIPARC:UPI00000299F3; GB:U08030; NID:g468254; PIDN:AAA19602.1; PID:

C:Comment: Expression of this protein is bladder-specific.

C:Genetics:

A:Gene: UPII

A:Introns: 26/1; 70/1; 116/2; 140/1

C:Keywords: glycoprotein; transmembrane protein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-84/Domain: propeptide #status predicted <PRO>

F:85-184/Product: uroplakin II #status predicted <WAT>

F:156-178/Domain: transmembrane #status predicted <TMM>

F:108/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 78.6%; Score 44; DB 2; Length 184;
 Best Local Similarity 87.5%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCH 8

Db 45 LIALPPCH 52

RESULT 38

JC7839
urolaklin II protein - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C:Accession: JC7839
R;Kwon, D.N.; Seo, H.G.; Kim, J.H.
Biochem. Biophys. Res. Commun. 293, 862-869, 2002
A:Title: Cloning, sequencing, and expression analysis of the porcine urolaklin II gene.
A:Reference number: JC7839; MUID:22050105; PMID:12054551
A:Accession: JC7839
A:Molecule type: DNA
A:Residues: 1-184 <KWO>
A:Cross-references: UNIPROT:Q95L04; UNIPARC:UPI000017CE44; GB:AY044180
C:Comment: This protein with only one transmembrane domain, belongs to a group of integrin roles in both kidney and bladder.
C:Genetics:
A:Gene: upi1
A:Introns: 26/1; 70/1; 116/2; 140/1

Query Match 78.6%; Score 44; DB 2; Length 184;
Best Local Similarity 87.5%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

Db 45 LVALPPCH 52

RESULT 39

A49713
urolaklin II precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A49713
R;Lin, J.H.; Wu, X.R.; Kreibich, G.; Sun, T.T.
J. Biol. Chem. 269, 1775-1784, 1994
A:Title: Precursor sequence, processing, and urothelium-specific expression of a major urolaklin II precursor.
A:Reference number: A49713; MUID:94124519; PMID:7507484
A:Accession: A49713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-185 <LIN>
A:Cross-references: UNIPROT:Q08537; UNIPARC:UPI0000137CD1; GB:L20633; NID:g304233; PIDN:
C:Keywords: glycoprotein; membrane bound; transmembrane protein

Query Match 78.6%; Score 44; DB 2; Length 185;
Best Local Similarity 87.5%; Pred. No. 1.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

Db 46 LVALPPCH 53

RESULT 40

YXBYT
thymidylate synthase (EC 2.1.1.45) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O2950; protein YOR074c
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1993 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C:Accession: S66957; A29546
R;Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66957
A:Accession: S66957
A:Molecule type: DNA
A:Residues: 1-259 <BOH>
A:Cross-references: UNIPROT:P06785; UNIPARC:UPI0000168414; EMBL:Z74982; NID:g1420228; PIDN:
A:Experimental source: strain S288C
R;Taylor, G.R.; Lagosky, P.A.; Storms, R.K.; Haynes, R.H.
J. Biol. Chem. 262, 5298-5307, 1987

A:Title: Molecular characterization of the cell cycle-regulated thymidylate synthase gene.
A:Reference number: A29546; MUID:87165970; PMID:3031048
A:Accession: A29546
A:Molecule type: DNA
A:Residues: 1-33, 'GTLSLFPAPQLRFSLRDTPFLTTTKVTRGIIILLWFLAGDT', 34-259 <TAY>
A:Cross-references: UNIPARC:UPI00001378F4; GB:J02706; NID:g172989; PIDN:AAA60940.1; PID:
C:Genetics:
A:Gene: SGD: CDC21; TMP1; MIPS:YOR074C
A:Cross-references: SGD:S0005600; MIPS:YOR074C
A:Map position: 15R
A:Introns: 34/1

C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; homodimer; methyltransferase; nucleus; py
F;10-259/Domain: thymidylate synthase homology <TDS>
F;132/Active site: Cys #status predicted

Query Match 78.6%; Score 44; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8

Db 127 MALPPCH 133

RESULT 41

SYBPT4
thymidylate synthase (EC 2.1.1.45) - phage T4
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
C:Accession: A00550; T10129
R;Chu, F.K.; Maley, G.F.; Maley, F.; Belfort, M.
Proc. Natl. Acad. Sci. U.S.A. 81, 3049-3053, 1984
A:Title: Intervening sequence in the thymidylate synthase gene of bacteriophage T4.
A:Reference number: A00550; MUID:84221902; PMID:6328492
A:Accession: A00550
A:Molecule type: DNA
A:Residues: 1-286 <CHU>
A:Cross-references: UNIPROT:P00471; UNIPARC:UPI000005CDB8; GB:K01804
R;Chu, F.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z16963
A:Accession: T10129
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-31, 'T', 33-286 <CH2>
A:Cross-references: UNIPARC:UPI000016D7A9; EMBL:M12742; NID:g3033366; PID:g3033367
A:Experimental source: strain alc4
C:Comment: This enzyme is also expressed by the thyA gene of E. coli; the phage and hos

C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F;1-286/Domain: thymidylate synthase homology <TDS>
F;156/Active site: Cys #status experimental

Query Match 78.6%; Score 44; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8

Db 151 MALPPCH 157

RESULT 42

SYBEHS
thymidylate synthase (EC 2.1.1.45) - saimirine herpesvirus 1
C:Species: saimirine herpesvirus 1
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 05-Oct-2004
C:Accession: A26269
R;Hones, R.W.; Bodemer, W.; Cameron, K.R.; Niller, H.H.; Fleckenstein, B.; Randall, R.

Proc. Natl. Acad. Sci. U.S.A. 83, 3604-3608, 1986
 A;Title: The A-T-rich genome of Herpesvirus saimiri contains a highly conserved gene for
 A;Reference number: A36269; MUID:86233282; PMID:3012520
 A;Accession: A36269

A;Molecule type: DNA

A;Residues: 1-294 <ON>
 A;Cross-references: UNIPARC:UPI00001378D3; GB:M13190; NID:g331074; PIDN:AAA46175.1; PID:
 C;Superfamily: thymidylate synthase; thymidylate synthase homology
 C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F;11-294/Domain: thymidylate synthase homology <TDS>
 F;176/Active site: Cys #status predicted

Query Match 78.6%; Score 44; DB 1; Length 294;
 Best Local Similarity 77.8%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10

DB 171 MVLPPCHVL 179

RESULT 43

YXUNTP

thymidylate synthase (EC 2.1.1.45) - Pneumocystis carinii
 C;Species: Pneumocystis carinii
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
 C;Accession: A33720
 R;Edman, U.; Edman, J.C.; Lundgren, B.; Santi, D.V.

Proc. Natl. Acad. Sci. U.S.A. 86, 6503-6507, 1989
 A;Title: Isolation and expression of the Pneumocystis carinii thymidylate synthase gene.
 A;Reference number: A33720; MUID:89367277; PMID:2671992

A;Accession: A33720

A;Molecule type: DNA

A;Residues: 1-297 <EDM>
 A;Cross-references: UNIPROT:P13100; UNIPARC:UPI0000110C98; GB:M25415; NID:g169429; PIDN:
 C;Superfamily: thymidylate synthase; thymidylate synthase homology
 C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F;6-297/Domain: thymidylate synthase homology <TDS>
 F;173/Active site: Cys #status predicted

Query Match 78.6%; Score 44; DB 1; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8

DB 168 MALPPCH 174

RESULT 44

YXCKTA

thymidylate synthase (EC 2.1.1.45) - yeast (Candida albicans)
 C;Species: Candida albicans
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 05-Oct-2004
 C;Accession: A32805
 R;Singer, S.C.; Richards, C.A.; Ferone, R.; Benedict, D.; Ray, P.
 J. Bacteriol. 171, 1372-1378, 1989

A;Title: Cloning, purification, and properties of Candida albicans thymidylate synthase.
 A;Reference number: A32805; MUID:89155436; PMID:2646281

A;Accession: A32805

A;Molecule type: DNA

A;Residues: 1-315 <SIN>
 A;Cross-references: UNIPARC:UPI0000172300; GB:J04230; NID:g170935; PIDN:AAA34374.1; PID:
 C;Superfamily: thymidylate synthase; thymidylate synthase homology
 C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
 F;9-315/Domain: thymidylate synthase homology <TDS>
 F;176/Active site: Cys #status predicted

Query Match 78.6%; Score 44; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8

DB 171 MALPPCH 177

RESULT 45

S73842
 thymidylate synthase (EC 2.1.1.45) - Mycoplasma pneumoniae (strain ATCC 29342)
 N;Alternate names: hypothetical protein F10_off328
 C;Species: Mycoplasma pneumoniae
 A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C;Accession: S73842; S49072

R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73842

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-328 <HIM>

A;Cross-references: UNIPARC:UPI0000165F96; EMBL:AE000050; GB:U00089; NID:g1674197; PIDN:
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

R;Proft, T.; Herrmann, R.

Mol. Microbiol. 13, 337-348, 1994

A;Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae
 A;Reference number: S49039; MUID:95075318; PMID:7984111

A;Accession: S49072

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 204-244, 'P', 252, 'LSYGA', 258-259 <PRO>

A;Cross-references: UNIPARC:UPI000016FB3F; EMBL:Z32654; NID:g474094; PIDN:CAA83575.1; PI

A;Experimental source: clone F10-2C

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

C;Genetics:

A;Gene: thya

A;Genetic code: SGC3

C;Superfamily: thymidylate synthase; thymidylate synthase homology

C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase

F;42-328/Domain: thymidylate synthase homology <TDS>

Query Match 78.6%; Score 44; DB 2; Length 328;

Best Local Similarity 77.8%; Pred. No. 2.4;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10

DB 206 MLLPPCHSL 214

RESULT 46

T01684

dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - maize
 C;Species: Zea mays (maize)

C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004

C;Accession: T01684

R;Cox, K.M.; Robertson, D.; Fites, R.C.

submitted to the EMBL Data library, June 1998

A;Description: Cloning of a cDNA encoding the bifunctional dihydrofolate reductase-thymi

A;Reference number: Z14392

A;Accession: T01684

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-521 <COK>

A;Cross-references: UNIPROT:O81395; UNIPARC:UPI00001298A6; EMBL:AF073488; NID:g3309065;

C;Genetics:

A;Gene: DRTS

C;Superfamily: bifunctional dihydrofolate reductase/thymidylate synthase; thymidylate sy

C;Keywords: methyltransferase; NADP; oxidoreductase

F;238-521/Domain: thymidylate synthase homology <TDS>

Query Match 78.6%; Score 44; DB 2; Length 521;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8
|||
Db 398 MALPPCH 404

RESULT 47

T37719
thymidylate synthase-like DNA metabolism protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37719
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Lyne, M.H.
A:Title: The genome sequence of the fission yeast Schizosaccharomyces pombe
A:Reference number: Z21739
A:Accession: T37719
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-625 <MUR>
A:Cross-references: UNIPROT:Q9UT17; UNIPARC:UPI000006C106; EMBL:AL109770; PIDN:CAB52423
A:Experimental source: strain 972h-; cosmid c15E1
C:Genetics:
A:Gene: SPDB:SPAC15E1.04
A:Map position: 1

Query Match 78.6%; Score 44; DB 2; Length 625;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8
|||
Db 492 MALPPCH 498

RESULT 48

G82569
thymidylate synthase XP2332 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82569
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82569
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <SIM>
A:Cross-references: UNIPROT:Q9PB13; UNIPARC:UPI00001378F3; GB:AE004044; GB:AE003849; NID
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.B.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 76.8%; Score 43; DB 2; Length 264;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||
Db 141 MALVPCHAL 149

RESULT 49

B84981
thymidylate synthase (EC 2.1.1.45) [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: B84981
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: B84981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: UNIPARC:UPI000005ESA5; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: thyA; BU440
C:Superfamily: thymidylate synthase; thymidylate synthase homology
C:Keywords: methyltransferase

Query Match 76.8%; Score 43; DB 2; Length 264;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||
Db 141 MRLPPCHVL 149

RESULT 50

B90579
thymidylate synthase (ts) (tease) [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C:Accession: B90579
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: B90579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q98031; UNIPARC:UPI00001378E2; GB:AL445566; PID:g14089953;
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 5380
A:Genetic code: SG3
C:Superfamily: thymidylate synthase; thymidylate synthase homology

Query Match 76.8%; Score 43; DB 2; Length 286;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||
Db 165 MLLPPCHTL 173

Search completed: February 17, 2006, 02:44:29
Job time : 59 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:36:31 ; Search time 227 Seconds
(without alignments)
31.081 Million cell updates/sec

Title: US-10-734-049B-188
Perfect score: 56
Sequence: 1 LMALPPCHAL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	222	Q8C2H6_MOUSE	Q8C2H6 mus musculus
2	56	100.0	222	Q8C2R3_MOUSE	Q8C2R3 mus musculus
3	56	100.0	230	Q8WYK4_HUMAN	Q8WYK4 homo sapien
4	56	100.0	279	Q8WYK3_HUMAN	Q8WYK3 homo sapien
5	56	100.0	307	1_TYSY_MOUSE	P07607 mus musculus
6	56	100.0	307	1_TYSY_RAT	P45352 rattus norv
7	56	100.0	307	2_Q544L2_MOUSE	Q544L2 mus musculus
8	56	100.0	307	2_Q8VDV6_MOUSE	Q8VDV6 mus musculus
9	56	100.0	307	2_Q9D0H1_MOUSE	Q9D0H1 mus musculus
10	56	100.0	312	1_TYSY_HUMAN	P04818 homo sapien
11	56	100.0	313	2_Q53FB7_HUMAN	Q53FB7 homo sapien
12	56	100.0	313	2_Q53Y97_HUMAN	Q53Y97 homo sapien
13	56	100.0	318	2_Q6P045_BRARE	Q6P045 brachydanio
14	56	100.0	319	2_Q7ZU17_BRARE	Q7ZU17 brachydanio
15	56	100.0	319	2_Q9DGH5_BRARE	Q9DGH5 brachydanio
16	52	92.9	264	1_TYSY_AZOSE	Q5P233 azoarcus sp
17	52	92.9	264	1_TYSY_NEIMA	Q9J157 neisseria m
18	52	92.9	264	1_TYSY_NEIMB	Q9J172 neisseria m
19	52	92.9	264	1_TYSY_PSEAE	Q916F1 pseudomonas
20	52	92.9	264	2_Q5P732_NEIG1	Q5P732 neisseria g
21	52	92.9	265	1_TYSY_NEIGO	Q33380 neisseria g
22	52	92.9	266	1_TYSY_BIFLO	Q8G3T9 bifidobacte
23	52	92.9	316	2_Q91CH7_9ALPH	Q91CH7 macropodid
24	51	91.1	295	2_Q9E202_9ALPH	Q9E202 cercopithe
25	51	91.1	337	1_TYSY_HRV8	P90463 human herpe
26	49	87.5	264	1_TYSY_CHRVO	P90295 chromobacte
27	49	87.5	314	1_TYSY_LISIN	Q92ad4 listeria in
28	49	87.5	314	1_TYSY_LISMF	Q71yel1 listeria mo
29	49	87.5	314	1_TYSY_LISMO	Q8Y626 listeria mo
30	48	85.7	63	2_Q7T4R2_9GAMA	Q7T4R2 baboon gamm
31	48	85.7	124	2_Q8QY23_RTRV	Q8QY23 rana tigrin

32	48	85.7	263	1_TYSY_MYCBO	P67045 mycobacteri
33	48	85.7	263	1_TYSY_MYCTU	P67044 mycobacteri
34	48	85.7	264	1_TYSY_BACAM	P54081 bacillus am
35	48	85.7	264	1_TYSY_BACSU	P11044 bacillus su
36	48	85.7	264	1_TYSY_AGRTS	Q8u8d3 agrobacteri
37	48	85.7	264	1_TYSY_BDEBA	Q6md12 bdellovibri
38	48	85.7	264	1_TYSY_BRAJA	Q89g35 bradyrhizob
39	48	85.7	264	1_TYSY_BRUME	P67042 brucella me
40	48	85.7	264	1_TYSY_BRUSU	P67043 brucella su
41	48	85.7	264	1_TYSY_RHILO	Q98kh9 rhizobium l
42	48	85.7	264	1_TYSY_RHIME	Q92hq5 rhizobium m
43	48	85.7	264	1_TYSY_RHOPA	Q6n447 rhodopseudo
44	48	85.7	264	1_TYSY_RHOPA	Q6n447 rhodopseudo
45	48	85.7	266	1_TYSY_MYCLE	Q9cbw0 mycobacteri
46	48	85.7	266	1_TYSY_MYCPA	Q73vz2 mycobacteri
47	48	85.7	267	2_Q4NHC8_9M1CC	Q4nhc8 artrobacte
48	48	85.7	269	1_TYSY_PROAC	Q6a161 propionibac
49	48	85.7	277	2_Q76YC2_9CAUD	Q76yc2 bacterioph
50	48	85.7	279	1_TYSY_CAUCR	Q9a3h0 caulobacter
51	48	85.7	282	2_Q39238_9GAMA	Q39238 rheus monk
52	48	85.7	288	1_TYSY_MYCMO	Q6k1q6 mycoplasma
53	48	85.7	288	1_TYSY_ONYPE	Q6yct0 onion yello
54	48	85.7	288	2_Q7QDW7_ANOGA	Q7qdw7 anopheles 9
55	48	85.7	289	2_Q8QTF3_WSSV	Q8qtf3 white spot
56	48	85.7	289	2_Q91L16_WSSV	Q91l16 white spot
57	48	85.7	290	1_TYSY_HSVAT	P12462 herpesvirus
58	48	85.7	290	2_Q9VTJ6_9HERP	Q9vtj6 ateline her
59	48	85.7	291	2_Q8JKA4_9VIRU	Q8jka4 heliothis z
60	48	85.7	294	1_TYSI_ENCCU	Q82584 encephalito
61	48	85.7	294	1_TYSI_ENCCU	Q82584 encephalito
62	48	85.7	294	1_TYSY_ASCSU	Q8srg2 encephalito
63	48	85.7	301	1_TYSY_VZVD	P09249 varicella-z
64	48	85.7	301	2_Q6QCP2_HHV3	Q6qcp2 human herpe
65	48	85.7	316	1_TYSY_LACCA	P00469 lactobacill
66	48	85.7	316	1_TYSY_LACPL	Q88w05 lactobacill
67	48	85.7	317	1_TYSY_CRYNE	P45351 cryptococcu
68	48	85.7	317	1_TYSY_OCEIH	Q8egg0 oceanobacil
69	48	85.7	317	2_Q55KW0_CRYNE	Q55kw0 cryptococcu
70	48	85.7	317	2_Q5DGT4_SCHJA	Q5dgt4 schistosoma
71	48	85.7	318	1_TYSY_BACAN	Q81r23 bacillus an
72	48	85.7	318	1_TYSY_BACCI	Q738x7 bacillus ce
73	48	85.7	318	1_TYSY_BACCR	Q81e05 bacillus ce
74	48	85.7	318	1_TYSY_BACCH	Q63bv5 bacillus ce
75	48	85.7	318	1_TYSY_BACCK	Q6h3c7 bacillus th
76	48	85.7	318	2_Q4MHD2_BACCE	Q4mhd2 bacillus ce
77	48	85.7	321	1_TYSY_DROME	Q76511 drosophila
78	48	85.7	321	2_Q541C9_DROME	Q541c9 drosophila
79	48	85.7	333	2_Q53D48_9GAMA	Q53d48 macaca fusc
80	48	85.7	333	2_Q77V82_9GAMA	Q77v82 cercopithe
81	48	85.7	333	2_Q9J2M3_9GAMA	Q9j2m3 rheus monk
82	48	85.7	333	2_Q9WRT8_9GAMA	Q9wrt8 macaca mula
83	48	85.7	340	2_Q759Q4_ASHGO	Q759q4 ashaya goss
84	48	85.7	499	2_Q27551_CRYPV	Q27551 cryptospori
85	48	85.7	518	1_DRTS2_ARATH	Q05763 arabidopsis
86	48	85.7	519	1_DRTS1_ARATH	Q05762 arabidopsis
87	48	85.7	521	2_Q27552_CRYPV	Q27552 cryptospori
88	48	85.7	521	2_Q5CGA3_CRYHO	Q5cga3 cryptospori
89	48	85.7	528	1_DRTS_DAUCA	P45350 daucus caro
90	48	85.7	530	1_DRTS_SOYBN	P51820 glycine max
91	48	85.7	530	2_Q8L6F0_PEA	Q8l6f0 pisum sativ
92	48	85.7	531	2_Q5CPQ4_CRYPV	Q5cpq4 cryptospori
93	48	85.7	554	2_Q4PBV6_USTMA	Q4pbv6 ustilago ma
94	48	85.7	577	2_Q39687_DAUCA	Q39687 daucus caro
95	47	83.9	118	2_P90658_9APIC	P90658 theileria s
96	47	83.9	264	1_TYSY_COXBU	Q83bg2 coxiella bu
97	47	83.9	264	1_TYSY_METFL	Q9ram7 methylobac
98	47	83.9	264	1_TYSY_RHOBA	Q7uid0 rhodopirell
99	47	83.9	264	1_TYSY_WIGBR	Q8d2n4 wigleswort
100	47	83.9	264	2_Q4J0C0_AZQVI	Q4j0c0 azotobacter
101	47	83.9	266	1_TYSY_CORGL	Q8ns38 corynebacte
102	47	83.9	267	1_TYSY_COREF	Q8fr47 corynebacte
103	47	83.9	270	1_TYSY_CORDI	Q6n1f2 corynebacte
104	47	83.9	273	2_Q4JX59_CORJK	Q4jx59 corynebacte

105	47	83.9	289	1	TVSY_EHV2	Q89940	equine herp	178	44	78.6	260	1	TVSY_METCA	Q60382	methylcoccc
106	47	83.9	296	1	TVSY_AGAB1	Q9p4t7	agarius bi	179	44	78.6	264	1	TVSY_BARHE	Q6g2s8	bartonella
107	47	83.9	323	1	TVSY_BORBR	Q7wp13	borderella	180	44	78.6	264	1	TVSY_BARQU	Q6tfz91	bartonella
108	47	83.9	323	1	TVSY_BORPA	Q7w1a9	borderella	181	44	78.6	279	2	Q56EF7_9CAUD	Q56ef7	aromonas p
109	47	83.9	323	1	TVSY_BORPE	Q7vuc3	borderella	182	44	78.6	279	2	Q6QGJ5_BPT5	Q6ggj5	bacterioph
110	47	83.9	323	1	TVSY_BORPEK	Q8cn9	pseudomonas	183	44	78.6	279	2	Q6U996_9CAUD	Q6u996	bacterioph
111	47	83.9	323	1	TVSY_PSESM	Q87u14	pseudomonas	184	44	78.6	280	1	TVSY_AC1AD	Q6fer7	acinetobact
112	47	83.9	323	1	Q4ZLV5_PSESY	Q4zlv5	pseudomonas	185	44	78.6	285	1	TVSY_SYMTH	Q67jq1	enterobacte
113	47	83.9	323	2	Q4K480_PSEF5	Q4k480	pseudomonas	186	44	78.6	285	2	Q5QC60_9CAUD	Q5qc60	enterobacte
114	47	83.9	387	2	Q9RR67_DEIRA	Q9rr67	deinococcus	187	44	78.6	286	1	TVSY_BPT4	P00471	bacterioph
115	47	83.9	491	2	Q95NT2_TRYCR	Q95nt2	trypanosoma	188	44	78.6	286	2	Q7Y4M9_BPT2	Q7y4m9	bacterioph
116	47	83.9	491	2	Q95NY4_TRYCR	Q95ny4	trypanosoma	189	44	78.6	286	2	Q6X184_BPT6	Q6x184	bacterioph
117	47	83.9	491	2	Q963S7_9TRYP	Q963s7	trypanosoma	190	44	78.6	286	2	Q6X185_9CAUD	Q6x185	bacterioph
118	47	83.9	491	2	Q963S8_TRYCR	Q963s8	trypanosoma	191	44	78.6	286	2	Q6X186_9CAUD	Q6x186	bacterioph
119	47	83.9	491	2	Q95NI3_TRYCR	Q95ni3	trypanosoma	192	44	78.6	286	2	Q6X187_BPR03	Q6x187	bacterioph
120	47	83.9	491	2	Q95NS0_TRYCR	Q95ns0	trypanosoma	193	44	78.6	286	2	Q6X188_BPR27	Q6x188	bacterioph
121	47	83.9	491	2	Q95NX3_TRYCR	Q95nx3	trypanosoma	194	44	78.6	286	2	Q6X189_9CAUD	Q6x189	bacterioph
122	47	83.9	498	2	Q4XXZ2_PLACH	Q4xxz2	plasmodium	195	44	78.6	286	2	Q6X190_9CAUD	Q6x190	bacterioph
123	47	83.9	520	1	DRTS_LEIAM	P18126	leishmania	196	44	78.6	286	2	Q6X191_9CAUD	Q6x191	bacterioph
124	47	83.9	520	1	DRTS_LEIMA	P07382	leishmania	197	44	78.6	286	2	Q6X192_9CAUD	Q6x192	bacterioph
125	47	83.9	520	2	Q8MQV1_LEICH	Q8mqv1	leishmania	198	44	78.6	286	2	Q6X193_BPR32	Q6x193	bacterioph
126	47	83.9	520	2	Q8MOV3_LEIIN	Q8mov3	leishmania	199	44	78.6	286	2	Q7Y4R7_BPR69	Q7y4r7	bacterioph
127	47	83.9	520	2	Q8MXB7_LEITR	Q8mxb7	leishmania	200	44	78.6	287	1	TVSY_MYCPN	P78029	mycoplasma
128	47	83.9	520	2	Q8MXB8_LEITR	Q8mxb8	leishmania	201	44	78.6	294	1	TVSY_SHV21	P08854	saimirine
129	47	83.9	520	2	Q4QIZ1_LEIMA	Q4qiz1	leishmania	202	44	78.6	294	2	Q80BX9_9GAMA	Q80bk9	saimirine
130	47	83.9	521	1	DRTS_TRYCR	Q27793	trypanosoma	203	44	78.6	296	1	TVSY_ZYMO	Q92671	zymomonas m
131	47	83.9	521	2	Q8T5T8_TRYCR	Q8t5t8	trypanosoma	204	44	78.6	296	2	Q6CCB3_YARLI	P6ccb3	yarrowia li
132	47	83.9	521	2	Q8T5T9_TRYCR	Q8t5t9	trypanosoma	205	44	78.6	297	1	TVSY_PNECA	P3100	pneumocysti
133	47	83.9	522	2	Q4N262_THEPA	Q4n262	theileria p	206	44	78.6	308	2	Q6FMT1_CANGA	Q6fmt1	candida gla
134	47	83.9	523	2	Q4U9G5_THEAN	Q4u9g5	theileria a	207	44	78.6	304	1	TVSY_VEAST	P06785	saccharomyc
135	47	83.9	583	1	DRTS_PLACH	P20712	plasmodium	208	44	78.6	312	2	Q6CXJ0_KLULA	Q6cxj0	kluyveromyc
136	47	83.9	585	2	Q4YWH2_PLABE	Q4ywh2	plasmodium	209	44	78.6	314	1	TVSY_CANAL	P12461	candida alb
137	47	83.9	587	1	DRTS_PLABA	Q27713	plasmodium	210	44	78.6	314	2	Q8MVZ9_9EUKA	Q8mvz9	cercomonas
138	47	83.9	588	2	Q95UH7_PLAYO	Q95uh7	plasmodium	211	44	78.6	315	2	Q59ZH0_CANAL	Q59zh0	candida alb
139	47	83.9	589	2	Q95SU9_PLAGA	Q95su9	plasmodium	212	44	78.6	316	2	Q6BV16_DEBHA	Q6bv16	debaromyce
140	47	83.9	608	1	DRTS_PLAFK	P13922	plasmodium	213	44	78.6	327	2	Q4TMD1_SPHN	Q4tmd1	erythroba
141	47	83.9	608	2	Q81R6_PLAF7	Q81r6	plasmodium	214	44	78.6	339	2	Q51UM7_WAGGR	Q51um7	magnaporthe
142	47	83.9	610	1	DRTS_TOXGO	Q07422	toxoplasma	215	44	78.6	344	2	Q4W9N9_ASFPU	Q4w9n9	aspergillus
143	47	83.9	623	1	DRTS_PLAVI	Q02604	plasmodium	216	44	78.6	511	2	Q7Z0Z9_BABBO	Q7z0z9	babesia bo
144	46	82.1	153	2	Q92IG0_ENTFA	Q92ig0	enterococc	217	44	78.6	521	1	DRTS_MAIZE	O81395	zea mays (m
145	46	82.1	295	1	Q9WB13_IRV6	Q9wb13	chilo iride	218	44	78.6	625	2	Q9UTI7_SCHPO	Q9uti7	schizosacch
146	46	82.1	315	1	TVSY_ENTFA	Q834r3	enterococc	219	44	78.6	654	2	Q5AXF2_EMENI	Q5axf2	aspergillus
147	46	82.1	318	1	TVSY_STAAC	Q5hfz6	staphylococ	220	43	76.8	213	2	Q6WT43_9PREM	Q6wt43	nanophyetus
148	46	82.1	318	1	TVSY_STAAM	P67046	staphylococ	221	43	76.8	213	2	Q6WT44_9PREM	Q6wt44	nanophyetus
149	46	82.1	318	1	TVSY_STAAN	P67047	staphylococ	222	43	76.8	213	2	Q6WT47_9PREM	Q6wt47	nanophyetus
150	46	82.1	318	1	TVSY_STAAR	Q6gg90	staphylococ	223	43	76.8	213	2	Q6WT48_9PREM	Q6wt48	nanophyetus
151	46	82.1	318	1	TVSY_STAAS	Q6gg9d4	staphylococ	224	43	76.8	213	2	Q6WT49_9PREM	Q6wt49	nanophyetus
152	46	82.1	318	1	TVSY_STAAT	P040m5	staphylococ	225	43	76.8	213	2	Q6WT79_9PREM	Q6wt79	nanophyetus
153	46	82.1	318	1	TVSY_STAAT	P67048	staphylococ	226	43	76.8	213	2	Q6WT79_9PREM	Q6wt79	nanophyetus
154	46	82.1	318	1	TVSY_STAAP	P080m4	staphylococ	227	43	76.8	213	2	Q6WT80_9PREM	Q6wt80	nanophyetus
155	46	82.1	318	1	TVSY_STAAP	Q5hmp6	staphylococ	228	43	76.8	213	2	Q6WT97_9PREM	Q6wt97	nanophyetus
156	46	82.1	318	2	Q7BMG2_STAUA	Q7bmg2	staphylococ	229	43	76.8	213	2	Q6WTA0_9PREM	Q6wta0	nanophyetus
157	46	82.1	318	2	Q7DI59_STAEP	Q7di59	staphylococ	230	43	76.8	213	2	Q6WTA1_9PREM	Q6wta1	nanophyetus
158	46	82.1	318	2	Q4L6D7_STAHL	Q4l6d7	staphylococ	231	43	76.8	213	2	Q6WTA7_9PREM	Q6wta7	nanophyetus
159	46	82.1	462	1	DRTS_PARTE	Q27828	paramesium	232	43	76.8	213	2	Q6WTC0_9PREM	Q6wtc0	nanophyetus
160	45	80.4	274	1	TVSY_PRAFT	Q5nfk5	francisella	233	43	76.8	213	2	Q6WTC7_9PREM	Q6wtc7	nanophyetus
161	45	80.4	289	1	TVSY_MYCGA	Q9xc19	mycoplasma	234	43	76.8	264	1	TVSY_BUCAL	P57515	buchnera ap
162	45	80.4	527	1	DRTS_TRYBB	Q27783	trypanosoma	235	43	76.8	264	1	TVSY_LEGPA	Q5x119	legionella
163	45	80.4	527	2	Q5B2G3_9TRYP	Q5b2g3	trypanosoma	236	43	76.8	289	1	TVSY_LEGPH	Q5xrl3	legionella
164	44	78.6	61	2	Q57NB3_SALCH	Q57nb3	salmonella	237	43	76.8	264	1	TVSY_LEGPH	Q5wsu5	legionella
165	44	78.6	65	2	Q6WEB0_9EUKA	Q6web0	hartmannell	238	43	76.8	264	1	TVSY_RALSO	Q8y0u6	raletonia s
166	44	78.6	65	2	Q8NV96_MASBA	Q8nv96	mastigamoeb	239	43	76.8	264	1	TVSY_XYLPF	Q8y0u6	raletonia s
167	44	78.6	89	2	Q9UEE8_HUMAN	Q9uee8	homo sapien	240	43	76.8	264	1	TVSY_XYLPF	Q8y0u6	raletonia s
168	44	78.6	109	2	Q9BMD8_BABBO	Q9bmd8	babesia bov	241	43	76.8	264	1	TVSY_MYCPU	Q8y0u6	raletonia s
169	44	78.6	151	2	Q9TU13_RABIT	Q9tu13	oryctolagus	242	43	76.8	289	1	TVSY_MYCPU	Q8y0u6	raletonia s
170	44	78.6	166	2	Q6X183_9CAUD	Q6x183	bacterioph	243	43	76.8	289	1	TVSY_MYCPU	Q8y0u6	raletonia s
171	44	78.6	184	1	UPK2_HUMAN	Q00526	homo sapien	244	43	76.8	318	1	TVSY_LACUO	Q74iu3	lactobacill
172	44	78.6	184	1	UPK2_MOUSE	P38575	mus musculu	245	43	76.8	488	2	Q8SCS7_9CAUD	Q8scs7	pseudomonas
173	44	78.6	184	1	UPK2_PIG	Q95104	sus scrofa	246	43	76.8	600	2	Q92PMO_RHIME	Q92pm0	rhizobium m
174	44	78.6	184	2	Q53YV0_HUMAN	Q53yv0	homo sapien	247	42	75.0	264	1	TVSY_BACFR	Q64pv5	bacteroides
175	44	78.6	184	2	Q5TUP8_PIG	Q5tup8	sus scrofa	248	42	75.0	264	1	TVSY_BACFR	Q8a639	bacteroides
176	44	78.6	185	1	UPK2_BOVIN	Q08537	bos taurus	249	42	75.0	264	2	Q5L9L6_BACFN	Q5l9l6	bacteroides
177	44	78.6	207	2	Q6WEA9_9EUKA	Q6wea9	corallochyt	250	42	75.0	300	2	Q4FQ50_9GAMM	Q4fq50	psychrobact

251	42	75.0	312	2	Q9N588_CABEL	Q9N588	caenorhabdi	324	38	67.9	299	2	Q6KGF1_9CAUD	Q6kcf1	bacterioph
252	42	75.0	315	2	Q60TX6_CABER	Q60tx6	caenorhabdi	325	38	67.9	395	2	Q510R9_PSEAE	Q510r9	pseudomonas
253	42	75.0	315	2	Q9Y052_CABEL	Q9y052	caenorhabdi	326	38	67.9	475	2	Q5VMS0_ORYSA	Q5vms0	oryza sativ
254	42	75.0	389	2	Q611Z9_CABER	Q611z9	caenorhabdi	327	38	67.9	1434	2	Q7QHC2_ANOGA	Q7qhc2	anopheles g
255	42	75.0	280	2	Q4QAU0_LEIMA	Q4qau0	leichmania	328	37	66.1	196	2	Q4XIU8_PLACH	Q4xiu8	plasmodium
256	41	73.2	287	1	TYSY_MTCGE	P47469	mycoplasma	329	37	66.1	220	1	RNH2_BRUAB	Q57ex6	brucella ab
257	41	73.2	318	1	TYSY_LACAC	Q5fk16	lactobacill	330	37	66.1	220	1	RNH2_BRUSE	P04ad9	brucella me
258	41	73.2	584	2	Q4SP22_TETNG	Q4sp22	tetradon n	331	37	66.1	220	1	RNH2_BRUSE	P04ad9	brucella me
259	40.5	72.3	513	2	Q5TBD6_HUMAN	Q5tbd6	homo sapien	332	37	66.1	256	2	Q51ZL9_MAGRV	Q51z19	magnaporthe
260	40.5	72.3	551	1	KIF12_HUMAN	Q96fn5	homo sapien	333	37	66.1	275	2	Q43476_HORVU	Q43476	hordeum vul
261	40.5	72.3	646	2	Q5TBE0_HUMAN	Q5tbe0	homo sapien	334	37	66.1	369	2	Q7XEC2_ORYSA	Q7xec2	oryza sativ
262	40	71.4	168	2	Q6RPO0_ORYSA	Q6rpo0	oryza sativ	335	37	66.1	424	2	Q4P8W6_USTNA	Q4p8w6	ustilago ma
263	40	71.4	264	1	TYSY_BACSK	Q9k7b5	bacillus ha	336	37	66.1	451	2	Q9W081_DROME	Q9w081	drosophila
264	40	71.4	264	1	TYSY_BACSK	Q5wd81	bacillus cl	337	37	66.1	500	2	Q7XEC7_ORYSA	Q7xec7	oryza sativ
265	40	71.4	264	1	TYSY_ECO57	P0a886	escherichia	338	37	66.1	720	2	Q51102_MAGGR	Q51102	magnaporthe
266	40	71.4	264	1	TYSY_ECOL6	P0a885	escherichia	339	37	66.1	956	2	Q81D95_PLAP7	Q81d95	plasmodium
267	40	71.4	264	1	TYSY_ECOLI	P0a884	escherichia	340	37	66.1	960	2	Q84Q44_ORYSA	Q84q44	oryza sativ
268	40	71.4	264	1	TYSY_ERWCT	Q6d816	erwinia car	341	37	66.1	963	2	Q7RQK2_PLAYO	Q7rqk2	plasmodium
269	40	71.4	264	1	TYSY_PHOLL	Q7n8u4	photorhabdu	342	37	66.1	966	2	Q4YTS5_PLABE	Q4yts5	plasmodium
270	40	71.4	264	1	TYSY_SALPA	Q5pen6	salmonella	343	36.5	65.2	584	2	Q583W8_9TRYP	Q583w8	trypanosoma
271	40	71.4	264	1	TYSY_SALPA	Q82412	salmonella	344	36	64.3	88	2	Q4MVR4_BACCE	Q4mvr4	bacillus ce
272	40	71.4	264	1	TYSY_SALTY	Q82na9	salmonella	345	36	64.3	140	2	Q51NP2_MAGGR	Q51np2	magnaporthe
273	40	71.4	264	1	TYSY_SHEON	Q8eb94	shewanella	346	36	64.3	146	2	Q52PB5_HUMAN	Q52pb5	homo sapien
274	40	71.4	264	1	TYSY_SHIFL	P48464	shigella fl	347	36	64.3	175	2	Q88IJ2_PSEPK	Q88ij2	pseudomonas
275	40	71.4	264	1	TYSY_XANAC	Q8pp46	xanthomonas	348	36	64.3	199	2	Q5EBG8_MOUSE	Q5ebg8	mus musculu
276	40	71.4	264	1	TYSY_XANCP	Q8pce7	xanthomonas	349	36	64.3	237	2	Q9W4G5_DROME	Q9w4g5	drosophila
277	40	71.4	264	1	TYSY_XANOR	Q5gwb5	xanthomonas	350	36	64.3	238	2	Q4V5M9_DROME	Q4v5m9	drosophila
278	40	71.4	264	1	TYSY_XENNE	Q6reu8	xenorhabdus	351	36	64.3	238	2	Q651K0_ORYSA	Q651k0	oryza sativ
279	40	71.4	264	1	TYSY_YERPE	Q8zhv1	yersinia pe	352	36	64.3	240	2	Q4S953_CABEL	Q4s953	caenorhabdi
280	40	71.4	264	1	TYSY_YERPS	Q66f19	yersinia ps	353	36	64.3	255	2	Q5NAE2_ORYSA	Q5nae2	oryza sativ
281	40	71.4	264	2	Q57KB6_SALCH	Q9wkb6	salmonella	354	36	64.3	259	2	Q92M31_RHIME	Q92m31	rhizobium m
282	40	71.4	264	2	Q8GMW7_ECOLI	Q8gmw7	escherichia	355	36	64.3	264	1	TYSY_BUCAP	Q8k9c3	buchnera ap
283	40	71.4	264	2	Q4UR35_XANCP	Q5vlp17	nocardia fa	356	36	64.3	264	2	Q67MJ1_SYMTD	Q5y3p6	rhizostoma
284	40	71.4	266	1	TYSY_NOCFA	Q5vlp17	nocardia fa	357	36	64.3	273	2	Q98GX3_RHITO	Q67mj1	symbiobacte
285	40	71.4	269	1	TYSY_LBIXX	Q6af10	leifsonia x	358	36	64.3	273	2	Q98GX3_RHITO	Q98gx3	rhizobium l
286	40	71.4	288	1	TYSY_MESFL	Q6fi45	mesoplasma	359	36	64.3	311	2	Q5ZJN6_CHICK	Q5zjnc6	gallus gall
287	40	71.4	300	2	Q6WIC0_BPKV4	Q6wic0	bacterioph	360	36	64.3	322	2	Q5ZHT8_CHICK	Q5zht8	gallus gall
288	40	71.4	307	2	Q9NDD3_TRISP	Q9ndd3	trichinella	361	36	64.3	358	1	MTG2_HABGA	P25283	haemophilus n
289	40	71.4	325	2	Q41NZ5_GIBZE	Q41nz5	gibberella	362	36	64.3	366	2	Q4RDL2_TETNG	Q4rld2	tetradon n
290	40	71.4	331	2	Q5TX45_ANOGA	Q5tx45	anopheles g	363	36	64.3	375	2	Q5SWQ0_CRYNE	Q5swq0	cryptococcu
291	40	71.4	368	2	Q7S072_NEUCR	Q7s072	neurospora	364	36	64.3	375	2	Q5KJ77_CRYNE	Q5kjj7	cryptococcu
292	40	71.4	673	2	Q4S708_TETNG	Q4s708	tetradon n	365	36	64.3	376	2	Q520P2_MAGGR	Q520p2	magnaporthe
293	39	69.6	69	2	Q69UK3_ORYSA	Q69uk3	oryza sativ	366	36	64.3	411	2	Q7PVK0_ANOGA	Q7pvk0	anopheles g
294	39	69.6	76	2	Q4SFN18_GLUOX	Q4sf18	gluconobact	367	36	64.3	420	2	Q61NW3_XENIA	Q61nw3	xenopus lae
295	39	69.6	94	2	Q4G3U6_TETNG	Q4g3u6	tetradon n	368	36	64.3	435	2	Q66IH1_XENTR	Q66ih1	xenopus tro
296	39	69.6	106	2	Q8C5H5_MOUSE	Q8c5h5	mus musculu	369	36	64.3	507	2	Q5FSV3_GLUOX	Q5fsv3	gluconobact
297	39	69.6	146	2	Q6FXG7_CANGA	Q6fxg7	candida gla	370	36	64.3	537	1	Q4QOH5_LEIMA	Q4qoh5	leishmania
298	39	69.6	196	2	Q5LSJ8_SILPO	Q5lsj8	silicibacte	371	36	64.3	559	1	FZD1_XENLA	Q9i3m5	xenopus lae
299	39	69.6	213	2	Q6WT45_9TREM	Q6wt45	nanophyetus	372	36	64.3	563	2	Q5UQG3_MIMIV	Q5uqg3	gallus gall
300	39	69.6	264	1	TYSY_GROKA	Q5kz25	geobacillus	373	36	64.3	592	1	FZD1_CHICK	Q57328	gallus gall
301	39	69.6	281	1	Q4SL59_TETNG	Q4sl59	tetradon n	374	36	64.3	635	1	MUTL_YERPE	Q8ziw4	yersinia pe
302	39	69.6	286	2	Q678J8_9VIRU	Q678j8	lymphocysti	375	36	64.3	635	2	Q66FB7_YERPS	Q66fb7	yersinia ps
303	39	69.6	336	2	Q18839_CABER	Q18839	caenorhabdi	376	36	64.3	641	1	FZD1_RAT	Q08463	rattus norv
304	39	69.6	371	2	Q934U8_SALTY	Q934u8	salmonella	377	36	64.3	642	1	FZD1_MOUSE	Q08421	mus musculu
305	39	69.6	395	2	Q6P625_XENTR	Q6p625	xenopus tro	378	36	64.3	642	2	Q7TS82_MOUSE	Q7ts82	mus musculu
306	39	69.6	475	2	Q6N733_RHOFA	Q6n733	rhodopseudo	379	36	64.3	647	2	Q549T8_HUMAN	Q549t8	homo sapien
307	39	69.6	853	2	Q8CDU5_MOUSE	Q8cdus	mus musculu	380	36	64.3	933	2	FZD1_HUMAN	Q5up38	homo sapien
308	39	69.6	111	2	Q4IX10_AZOVI	Q4ix10	azotobacter	381	36	64.3	826	2	Q4SMX1_TETNG	Q4smx1	tetradon n
309	38	67.9	122	1	RNPA_STYP6	Q5n605	synecococc	382	36	64.3	827	2	Q7G4Z1_ORYSA	Q7g4z1	oryza sativ
310	38	67.9	131	2	Q9CUM2_MOUSE	Q9cum2	mus musculu	383	36	64.3	916	2	Q53QT2_HUMAN	Q53qt2	homo sapien
311	38	67.9	142	1	TAKIL_MOUSE	P58500	mus musculu	384	36	64.3	933	1	PERT_HUMAN	P07202	homo sapien
312	38	67.9	142	2	Q8TCLF_HUMAN	Q8tcl9	homo sapien	385	36	64.3	933	2	Q502Y3_HUMAN	Q502y3	homo sapien
313	38	67.9	142	2	Q6DGF7_RAT	Q6dgf7	rattus norv	386	36	64.3	992	1	POLS_RUBVM	P08563	rubella vir
314	38	67.9	142	2	Q544C0_MOUSE	Q544c0	mus musculu	387	36	64.3	1063	2	POLS_RUBVH	P21480	rubella vir
315	38	67.9	143	2	Q7XXY9_GRIJA	Q7xyy9	griffithsia	388	36	64.3	1222	2	Q9VAT1_DROME	Q9vat1	drosophila
316	38	67.9	231	2	Q53VY5_THET8	Q53vy5	thermus the	389	36	64.3	1899	2	Q9XEG1_GOSHI	Q9xeg1	gossypium h
317	38	67.9	233	2	Q8Y9A7_LISMO	Q8y9a7	listeria mo	390	36	64.3	4725	1	DYHC_DICDI	P34036	dicyosteli
318	38	67.9	233	2	Q92E27_LISIN	Q92e27	listeria mo	391	36	64.3	4730	2	Q8T128_DICDI	Q8t128	dicyosteli
319	38	67.9	233	2	Q722S5_LISMF	Q722s5	listeria mo	392	35	62.5	55	2	Q4HSK7_CAMUP	Q4hsk7	campylobact
320	38	67.9	242	1	TAKIL_HUMAN	P57077	homo sapien	393	35	62.5	127	2	Q9CTG5_MOUSE	Q9ctg5	mus musculu
321	38	67.9	264	1	TYSY_BUCBP	P59427	buchnera ap	394	35	62.5	129	2	Q7TNN1_MOUSE	Q7tnn1	mus musculu
322	38	67.9	264	1	TYSY_PORGI	Q7mcb5	porphyromon	395	35	62.5	134	2	Q93X70_SORBI	Q93x70	sorghum bic
323	38	67.9	292	2	Q9YVK4_MSEPV	Q9yyvk4	melanoplus	396	35	62.5	136	2	Q88FL4_PSEPK	Q88fl4	pseudomonas

337	35	62.5	147	2	Q6BL85_DREHA	Q6bl85 debaryomyce	470	35	62.5	926	1	PERT_PIG	P05933 sus scrofa
338	35	62.5	152	2	Q9YHE9_CYPCA	Q9Yhe9 cyprinus ca	471	35	62.5	965	2	Q4WN16_ASPFU	Q4wny6 aspergillus
339	35	62.5	157	2	Q96DN7_HUMAN	Q96dn7 homo sapien	472	35	62.5	966	2	Q7PQX6_ANOGA	Q7pqx6 anopheles g
400	35	62.5	159	2	Q41KA1_9URUK	Q41ka1 burkholderi	473	35	62.5	967	2	Q9BJZ5_DROME	Q9bjz5 drosophila
401	35	62.5	163	2	Q4NWG2_9DELT	Q4nwg2 anaeromyxob	474	35	62.5	988	2	Q97867_PIG	Q97867 sus scrofa
402	35	62.5	167	2	Q903P0_CHICK	Q903p0 gallus gall	475	35	62.5	999	2	Q4FYK5_LEIMA	Q4fyk5 leishmania
403	35	62.5	170	2	Q90TDL_SCHPO	Q90tdl schizosacch	476	35	62.5	1116	2	Q8UBP7_AGR75	Q8ubp7 agrobacteri
404	35	62.5	178	2	Q61103_DROME	Q61103 drosophila	477	35	62.5	1121	2	Q6BD87_ARTGO	Q6bd87 arthrobacte
405	35	62.5	181	2	Q5JLS3_ORISA	Q5jls3 oryza sativ	478	35	62.5	1554	2	Q4SMT5_TETNG	Q4smt5 tetraodon n
406	35	62.5	185	2	Q5JLS3_ORISA	Q5jls3 oryza sativ	479	35	62.5	1624	2	Q9W437_DROME	Q9w437 drosophila
407	35	62.5	191	1	CRF_PIG	P06296 sus scrofa	480	35	62.5	1639	2	Q8Q4W6_FUGRU	Q8q4w6 fugu rubrip
408	35	62.5	195	2	Q96LW6_HUMAN	Q96lw6 homo sapien	481	35	62.5	1650	2	Q9QVT6_9MURI	Q9qvt6 rattus sp.
409	35	62.5	195	2	Q9N7A6_ORISA	Q9n7a6 oryza sativ	482	35	62.5	2042	2	Q8TZ07_METKA	Q8tz07 methanopyru
410	35	62.5	196	1	CRF_HUMAN	P08850 homo sapien	483	35	62.5	2196	2	Q4RT37_TETNG	Q4rt37 tetraodon n
411	35	62.5	202	2	Q00439_HUMAN	O00439 homo sapien	484	35	62.5	2286	2	Q4QHQ1_LEIMA	Q4qhql leishmania
412	35	62.5	204	2	Q72D71_DESVH	Q72d71 desulfovibr	485	35	62.5	3670	1	CSMD3_HUMAN	P98158 rattus norv
413	35	62.5	213	2	Q6WT51_9RTEK	Q6wt51 nanophyetus	486	35	62.5	4660	1	LAP2_RAT	Q5RGQ4 brachydanio
414	35	62.5	215	2	Q8TW85_METKA	Q8tw85 methanopyru	487	35	62.5	4864	2	Q5RGQ4_BRARE	Q5rgq4 brachydanio
415	35	62.5	226	2	Q8EYN9_SINPW	Q8eyn9 synecococc	488	35	62.5	5374	2	Q99ND0_MOUSE	Q99nd0 mus musculu
416	35	62.5	246	2	Q5JL26_ORISA	Q5jls26 oryza sativ	489	35	62.5	5376	1	ZAN_MOUSE	O88799 mus musculu
417	35	62.5	247	2	Q4RKZ7_TETNG	Q4rkz7 tetraodon n	490	34	60.7	49	2	Q80HS3_9VIRU	Q80hs3 hepatitis e
418	35	62.5	262	2	Q6NUN9_CORDI	Q6nun9 corynebacte	491	34	60.7	56	2	Q9KZL7_STRCO	Q9kzl7 streptomyce
419	35	62.5	264	1	TVSY_NITRU	Q82w3 nitrosomona	492	34	60.7	56	2	Q82DD3_STRAW	Q82dd3 streptomyce
420	35	62.5	285	2	Q56B75_9CAUD	Q56bv5 enterobacte	493	34	60.7	94	2	Q4X3B8_PLACH	Q4x3b8 plasmodium
421	35	62.5	296	2	Q7W9G3_BORPA	Q7w9g3 bordetella	494	34	60.7	114	2	Q4LES2_9VIRU	Q4les2 hepatitis e
422	35	62.5	296	2	Q7WH93_BORBR	Q7wh93 bordetella	495	34	60.7	114	2	Q4LES5_9VIRU	Q4les5 hepatitis e
423	35	62.5	297	2	Q7V9E3_PROMM	Q7v9e3 prochloroco	496	34	60.7	116	2	Q88GZ7_FSEPK	Q88gz7 pseudomonas
424	35	62.5	300	2	Q7UNIO_RHOBA	Q7uni0 rhodospirill	497	34	60.7	119	2	Q6YZK4_ORPSA	Q6yzk4 oryza sativ
425	35	62.5	309	1	KHSE_BACHD	Q9k7e4 bacillus ha	498	34	60.7	140	1	Y155_ARCFU	Q30082 archaeoglob
426	35	62.5	323	2	Q4LOA4_9URUK	Q4loa4 burkholderi	499	34	60.7	141	2	Q4J7V3_SULAC	Q4j7v3 sulfolobus
427	35	62.5	323	2	Q63S51_BURPS	Q63s51 burkholderi	500	34	60.7	141	2	Q8BN63_MOUSE	Q8bn63 mus musculu
428	35	62.5	323	2	Q62M70_HALVO	Q62m70 burkholderi	501	34	60.7	147	2	Q519V8_SORBI	Q519v8 sorghum bic
429	35	62.5	342	2	Q9UWQ5_BURPS	Q9uwq5 halobacteri	502	34	60.7	150	2	Q96MU0_HUMAN	Q96mu0 homo sapien
430	35	62.5	353	1	NLEX_HUMAN	Q9H913 homo sapien	503	34	60.7	151	2	Q8W344_HUMAN	Q8w344 mus musculu
431	35	62.5	353	1	Q64KA2_HUMAN	Q64ka2 homo sapien	504	34	60.7	151	2	Q9DA47_MOUSE	Q9da47 mus musculu
432	35	62.5	355	2	Q4LM44_9URUK	Q4lm44 burkholderi	505	34	60.7	152	2	Q5JY54_HUMAN	Q5jy54 homo sapien
433	35	62.5	358	1	TRMU_RICPR	Q98dm1 rickettsia	506	34	60.7	152	2	Q937A1_PSESD	Q937a1 pseudomonas
434	35	62.5	358	1	TRMU_RICPR	Q98d66 rickettsia	507	34	60.7	159	2	Q75QP2_RANCA	Q75qp2 rana catesb
435	35	62.5	358	2	Q7P3V6_FUSNV	Q7p3v6 fusobacteri	508	34	60.7	160	2	Q9HA58_HUMAN	Q9ha58 homo sapien
436	35	62.5	358	2	Q8REU7_FUSNV	Q8reu7 fusobacteri	509	34	60.7	162	2	Q8C3A5_MOUSE	Q8c3a5 mus musculu
437	35	62.5	363	2	Q7XEB6_ORISA	Q7xeb6 oryza sativ	510	34	60.7	164	2	Q8C3A5_MOUSE	Q8c3a5 mus musculu
438	35	62.5	370	2	Q5D975_SCHJA	Q5d975 schistosoma	511	34	60.7	168	2	Q5GH78_LAMFL	Q5gh78 lampetra fl
439	35	62.5	376	2	Q61GV1_CAEBR	Q61gv1 caenorhabdi	512	34	60.7	169	2	Q5GXL5_XANOR	Q5gxl5 xanthomonas
440	35	62.5	379	2	Q51WF2_MAGBR	Q51wf2 magnaporthe	513	34	60.7	169	2	Q7W364_BORPA	Q7w364 bordetella
441	35	62.5	383	2	Q7XRA0_ORISA	Q7xra0 oryza sativ	514	34	60.7	169	2	Q7WEI2_BORBR	Q7wei2 bordetella
442	35	62.5	386	2	Q4TS23_9SPHN	Q4ts23 erythrobact	515	34	60.7	185	2	Q8L2B6_BORPE	Q8l2b6 bordetella
443	35	62.5	396	1	KARG1_CABEL	Q10454 caenorhabdi	516	34	60.7	186	2	Q6ESQ9_ORISA	Q6esq9 oryza sativ
444	35	62.5	402	2	Q5LHA5_BACFN	Q5lha5 bacteroides	517	34	60.7	190	1	CRF_SHEEP	Q62rw3 homo sapien
445	35	62.5	402	2	Q64WE5_BACFN	Q64we5 bacteroides	518	34	60.7	190	1	CRF_SHEEP	Q95mi6 bos taurus
446	35	62.5	404	2	Q7PVJ9_ANOGA	Q7pvj9 anopheles g	519	34	60.7	192	2	Q6Z947_ORISA	Q6z947 oryza sativ
447	35	62.5	412	2	Q8S1V4_ORISA	Q8s1v4 oryza sativ	520	34	60.7	195	2	Q6ZU23_HUMAN	Q6zu23 homo sapien
448	35	62.5	424	2	Q60S23_CAEBR	Q60s23 caenorhabdi	521	34	60.7	203	2	Q8D712_VIBVU	Q8d712 vibrio vuln
449	35	62.5	444	2	Q20584_CABEL	Q20584 caenorhabdi	522	34	60.7	203	2	Q7MEZ8_VIBVU	Q7mez8 vibrio vuln
450	35	62.5	482	2	Q75KL2_ORISA	Q75kl2 oryza sativ	523	34	60.7	209	2	Q6J9L0_9PRIM	Q6j9l0 gorilla gor
451	35	62.5	490	2	Q4WAX0_ASPFU	Q4wax0 aspergillus	524	34	60.7	221	2	Q4I250_AZOV1	Q4i250 azotobacter
452	35	62.5	506	2	Q5N1V8_SINPW	Q5n1v8 synecococc	525	34	60.7	221	2	Q6LSA7_PHOPR	Q6lsa7 photobacter
453	35	62.5	515	1	DRTS_CRIFA	Q23695 crithidia f	526	34	60.7	259	2	Q4WN04_ASPFU	Q4wn04 aspergillus
454	35	62.5	515	2	Q4RW13_TETNG	Q4rw13 tetraodon n	527	34	60.7	263	2	Q4LTV9_9BURK	Q4ltv9 burkholderi
455	35	62.5	520	2	Q4NU92_9DELT	Q4nu92 anaeromyxob	528	34	60.7	263	2	Q4RSL3_TETNG	Q4rsl3 tetraodon n
456	35	62.5	521	2	Q6Q156_RAT	Q6q156 rattus norv	529	34	60.7	273	2	Q75H84_ORISA	Q75h84 oryza sativ
457	35	62.5	530	2	Q8S1B2_ORISA	Q8s1b2 oryza sativ	530	34	60.7	273	2	Q8XZ63_RALSO	Q8xz63 ralstonia s
458	35	62.5	557	2	Q9V7E0_DROME	Q9v7e0 drosophila	531	34	60.7	278	2	Q926C4_RHIME	Q926c4 rhizobium m
459	35	62.5	586	2	Q4NXL1_9DELT	Q4nxl1 anaeromyxob	532	34	60.7	287	2	Q6ZMD1_HUMAN	Q6zmdl homo sapien
460	35	62.5	590	2	Q8S5Y2_ORISA	Q8s5y2 oryza sativ	533	34	60.7	291	2	Q8MUJ6_9ASCI	Q8mvj6 boltonia vi
461	35	62.5	633	2	Q8MLA8_DROME	Q8mla8 drosophila	534	34	60.7	291	2	Q6OAI7_METCA	Q6oai7 methylococc
462	35	62.5	637	2	Q7FAB5_ORISA	Q7fab5 oryza sativ	535	34	60.7	292	2	Q5ONL4_ENTHI	Q5onl4 entamoeba h
463	35	62.5	639	1	FU11_YEAST	P38196 saccharomyc	536	34	60.7	293	2	Q919N5_BRARE	Q919n5 brachydanio
464	35	62.5	651	2	Q6D065_ERWCT	Q6d065 erwinia car	537	34	60.7	295	1	CHIO_RAT	Q03070 rattus norv
465	35	62.5	675	1	Y3064_ERWCT	Q6d2nl erwinia car	538	34	60.7	295	2	Q63XQ0_BURPS	Q63xq0 burkholderi
466	35	62.5	764	2	Q8LNU9_ORISA	Q8lnu9 oryza sativ	539	34	60.7	299	2	Q824Q1_CAEBR	Q824q1 caenorhabdi
467	35	62.5	771	2	Q6DE09_XENLA	Q6de09 xenopus lae	540	34	60.7	332	1	CHIO_MOUSE	Q80xdl mus musculu
468	35	62.5	831	2	Q4T505_TETNG	Q4t505 tetraodon n	541	34	60.7	332	2	Q6AUI5_ORISA	Q6aui5 oryza sativ
469	35	62.5	891	2	Q8MLA9_DROME	Q8mla9 drosophila	542	34	60.7	332	2	Q6GNI5_XENLA	Q6gni5 xenopus lae

543	34	60.7	345	2	Q4YU44_PLABE	Q4YU44 plasmodium	616	34	60.7	930	2	Q4QIF0_LEIMA	Q4qif0 leishmania
544	34	60.7	348	2	Q5W37_PLABE	Q5w37 plasmodium	617	34	60.7	936	2	Q4T3Z2_TETNG	Q4t3z2 tetragonia
545	34	60.7	349	2	Q7RFH4_PLAYO	Q7rfh4 plasmodium	618	34	60.7	969	2	Q8T3T3_TOXGO	Q8t3t3 toxoplasma
546	34	60.7	349	2	Q63611_BALCA	Q63611 balanogloss	619	34	60.7	969	2	Q5KQ11_MACFA	Q5kq11 macaca fasc
547	34	60.7	352	2	Q84SM1_ORISA	Q84sm1 oryza sativ	620	34	60.7	976	1	PDR3_YEAST	P33200 saccharomyc
548	34	60.7	352	2	Q50170_MYCLE	Q50170 mycobacteri	621	34	60.7	976	2	Q6BIF6_YEAST	Q6blf6 saccharomyc
549	34	60.7	368	2	Q9CBB8_MYCLE	Q9cbb8 mycobacteri	622	34	60.7	998	2	Q5B566_EMENI	Q5b566 aspergillus
550	34	60.7	377	2	Q51HP6_MAGGR	Q51hp6 magnaporthe	623	34	60.7	1005	2	Q5B566_EMENI	Q5b566 aspergillus
551	34	60.7	382	2	Q6EN39_ORISA	Q6en39 oryza sativ	624	34	60.7	1042	2	Q5KQ11_MACFA	Q5kq11 macaca fasc
552	34	60.7	385	2	Q7R786_PLAYO	Q7r786 plasmodium	625	34	60.7	1081	2	Q7SMU9_HUMAN	Q7smu9 homo sapien
553	34	60.7	398	2	Q7WAV2_BORPA	Q7wav2 bordeletia	626	34	60.7	1088	2	Q8N4D4_HUMAN	Q8n4d4 homo sapien
554	34	60.7	404	2	Q75BL2_ASHGO	Q75bl2 ashya goss	627	34	60.7	1088	2	Q7XIU5_ORISA	Q7xiu5 oryza sativ
555	34	60.7	411	2	Q96NU6_HUMAN	Q96nu6 homo sapien	628	34	60.7	1102	2	Q9ZVE4_ARATH	Q9zve4 arabidopsia
556	34	60.7	429	2	Q6ATU7_ORISA	Q6atu7 oryza sativ	629	34	60.7	1158	2	Q5JXY1_HUMAN	Q5jxy1 homo sapien
557	34	60.7	443	2	Q69T50_ORISA	Q69t50 oryza sativ	630	34	60.7	1169	1	AT132_MOUSE	Q9ctg6 mus musculu
558	34	60.7	450	2	Q4XVB7_PLACH	Q4xvb7 plasmodium	631	34	60.7	1175	2	Q6S9Z5_HUMAN	Q6s9z5 homo sapien
559	34	60.7	459	2	Q4SDD9_TETNG	Q4sdd9 tetraodon n	632	34	60.7	1180	1	AT132_HUMAN	Q9ngl1 homo sapien
560	34	60.7	464	2	Q5B6R1_EMENI	Q5b6r1 aspergillus	633	34	60.7	1239	2	Q83868_TREPA	Q83868 treponema p
561	34	60.7	465	2	Q6QP22_LACT	Q6qp22 lactococcus	634	34	60.7	1317	2	Q4P9E7_USTMA	Q4p9e7 ustilago ma
562	34	60.7	467	2	Q5VR75_ORISA	Q5vr75 oryza sativ	635	34	60.7	1392	2	Q6P9E7_USTMA	Q6p9e7 ustilago ma
563	34	60.7	467	2	Q84TY9_ORISA	Q84ty9 oryza sativ	636	34	60.7	1580	1	GLI3_HUMAN	P10071 homo sapien
564	34	60.7	468	1	CHIO_HUMAN	P52757 homo sapien	637	34	60.7	1580	1	GLI3_HUMAN	Q51s56 pan troglod
565	34	60.7	474	2	Q410J4_GIBZE	Q410j4 gibberella	638	34	60.7	1592	2	Q5KIF1_CRYNE	Q5kif1 cryptococcu
566	34	60.7	480	2	Q7NW92_CHRVO	Q7nw92 chromobacte	639	34	60.7	1592	2	Q5TY18_CRYNE	Q5ty18 cryptococcu
567	34	60.7	482	1	PAF53_MOUSE	Q8k202 mus musculu	640	34	60.7	1608	2	Q4UBT6_THEAN	Q4ubt6 theileria a
568	34	60.7	489	2	Q527H3_MAGGR	Q527h3 magnaporthe	641	34	60.7	1811	2	Q9QXN9_MOUSE	Q9qxn9 mus musculu
569	34	60.7	508	2	Q4XIV1_ASPFU	Q4xiv1 aspergillus	642	34	60.7	1862	2	Q83X88_STRRO	Q83x88 streptomyce
570	34	60.7	518	1	THI4_SCHPO	P40386 s probable	643	34	60.7	1878	2	Q5AJJ7_DICDI	Q541j7 dictyosteli
571	34	60.7	520	2	Q7X714_ORISA	Q7x714 oryza sativ	644	34	60.7	1986	2	Q9QXN0_MOUSE	Q9qxn0 mus musculu
572	34	60.7	523	2	Q4Q536_LEIMA	Q4q536 leishmania	645	34	60.7	1995	2	Q8TF72_HUMAN	Q8tf72 homo sapien
573	34	60.7	535	2	Q5JRM1_HUMAN	Q5jrm1 cryptooccu	646	34	60.7	2373	2	Q6XPA4_YERFR	Q6xpa4 yersinia fr
574	34	60.7	538	2	Q55V41_CRYNE	Q55v41 cryptooccu	647	34	60.7	2381	2	Q5TNW9_ANOGA	Q5tnw9 anopheles g
575	34	60.7	538	2	Q5KL40_CRYNE	Q5kl40 cryptooccu	648	34	60.7	2446	2	Q7PLZ8_ANOGA	Q7plz8 anopheles g
576	34	60.7	547	2	Q6ZRI8_HUMAN	Q6zri8 homo sapien	649	34	60.7	2458	2	Q4SIC2_TETNG	Q4sic2 tetraodon n
577	34	60.7	548	2	Q8AVJ9_XENLA	Q8avj9 xenopus lae	650	34	60.7	2908	2	Q7N4L0_PROLL	Q7n4l0 photorhabdu
578	34	60.7	548	2	Q5BL72_XENTR	Q5bl72 xenopus lae	651	34	60.7	6077	2	Q5BDY8_EMENI	Q5bdy8 aspergillus
579	34	60.7	549	1	FZD7_XENLA	Q9puk8 xenopus tro	652	34	60.7	7599	2	Q4IKE3_GIBZE	Q4ike3 gibberella
580	34	60.7	553	2	Q4T738_TETNG	Q4t738 tetraodon n	653	33	53.8	741	2	Q29065_ARCFU	Q29065 archaeoglob
581	34	60.7	559	2	Q90ZT3_BRARE	Q90zt3 brachydanio	654	33	58.9	50	2	Q8K3C7_MOUSE	Q8k3c7 mus musculu
582	34	60.7	559	2	Q98I2_BRARE	Q98i2 brachydanio	655	33	58.9	65	2	Q8S568_CATRO	Q8s568 catharanthu
583	34	60.7	559	2	Q6NV44_BRARE	Q6nv44 brachydanio	656	33	58.9	68	2	Q6Z8D6_ORISA	Q6z8d6 oryza sativ
584	34	60.7	559	2	Q7SZR7_BRARE	Q7s7r7 brachydanio	657	33	58.9	72	2	Q9F9K1_SULIS	Q9f9k1 sulfolobus
585	34	60.7	567	1	FZD7_CHICK	Q57329 gallus gall	658	33	58.9	73	2	Q5Z6C6_ORISA	Q5z6c6 oryza sativ
586	34	60.7	572	1	FZD7_MOUSE	Q6p551 mus musculu	659	33	58.9	79	2	Q50987_NEIGO	Q50987 neisseria g
587	34	60.7	572	1	Q6P551_MOUSE	Q6p551 mus musculu	660	33	58.9	80	2	Q7LGZ0_PHOPR	Q7lgz0 photobacter
588	34	60.7	574	1	FZD7_HUMAN	Q75084 homo sapien	661	33	58.9	81	2	Q7P547_FUSNV	Q7p547 fusobacteri
589	34	60.7	574	2	Q53S59_HUMAN	Q53s59 homo sapien	662	33	58.9	81	2	Q8RFL2_FUSNN	Q8rf12 fusobacteri
590	34	60.7	583	2	Q4QGT0_LEIMA	Q4qgt0 leishmania	663	33	58.9	85	2	Q27065_TRYRA	Q27065 trypanosoma
591	34	60.7	588	1	HD10_RAT	Q569c4 rattus norv	664	33	58.9	97	2	Q8CDY0_MOUSE	Q8cdy0 mus musculu
592	34	60.7	600	2	Q6TEM7_BRARE	Q6tem7 brachydanio	665	33	58.9	105	2	Q5J5E8_9CAUD	Q5j5e8 mycobacteri
593	34	60.7	603	2	Q4NTD7_9DELT	Q4ntd7 anaeromyxob	666	33	58.9	105	2	Q9B055_BPMB1	Q9b055 mycobacteri
594	34	60.7	626	2	Q4WY64_ASPFU	Q4wy64 aspergillus	667	33	58.9	109	2	Q5F578_NEIG1	Q5f578 neisseria g
595	34	60.7	636	1	LREN4_MOUSE	Q80x08 mus musculu	668	33	58.9	109	2	Q9JWN4_NEISSERIA	Q9jwn4 neisseria m
596	34	60.7	650	2	Q8CIJ9_MOUSE	Q8cij9 mus musculu	669	33	58.9	109	2	Q9KIP4_NEISSERIA	Q9kip4 neisseria m
597	34	60.7	666	1	HD10_MOUSE	Q6p3e7 mus musculu	670	33	58.9	111	2	Q5E554_VIBF1	Q5e554 vibrio floc
598	34	60.7	683	2	Q9VH19_DROME	Q9vh19 drosophila	671	33	58.9	117	2	Q74DC0_GEOSL	Q74dc0 geobacter s
599	34	60.7	727	2	Q4WRL9_ASPFU	Q4wrl9 aspergillus	672	33	58.9	123	2	Q7LMF4_HUMAN	Q7lmf4 homo sapien
600	34	60.7	733	2	Q8YCW2_BRUME	Q8ycw2 brucella me	673	33	58.9	124	2	Q72CB4_DSUVH	Q72cb4 deulfovibr
601	34	60.7	740	2	Q5JWV6_HUMAN	Q5jwv6 homo sapien	674	33	58.9	137	2	Q44402_9RHIZ	Q44402 agrobacteri
602	34	60.7	750	2	Q810L8_MOUSE	Q810l8 mus musculu	675	33	58.9	138	2	Q7XW04_ORISA	Q7xw04 oryza sativ
603	34	60.7	764	2	Q9HAP8_HUMAN	Q9hap8 homo sapien	676	33	58.9	143	2	Q4HA76_9DEIO	Q4ha76 deinococcu
604	34	60.7	776	2	Q41BX2_GIBZE	Q41bx2 gibberella	677	33	58.9	148	2	Q67NC0_SYMTH	Q67nc0 symbiobacte
605	34	60.7	778	1	NTRK1_CHICK	Q91009 gallus gall	678	33	58.9	149	2	Q64E07_9ARCH	Q64e07 uncultured
606	34	60.7	829	1	KSR2_HUMAN	Q6vab6 homo sapien	679	33	58.9	149	2	Q6VUB0_9ARCH	Q6vub0 uncultured
607	34	60.7	835	2	Q52EZ0_MAGGR	Q52ez0 magnaporthe	680	33	58.9	150	2	Q8BRQ5_MOUSE	Q8brq5 mus musculu
608	34	60.7	841	2	Q94HS2_ORISA	Q94hs2 oryza sativ	681	33	58.9	150	2	Q6TG13_BRARE	Q6tg13 brachydanio
609	34	60.7	841	2	Q7XGU0_ORISA	Q7xgu0 oryza sativ	682	33	58.9	156	2	Q8C6Q2_MOUSE	Q8c6q2 mus musculu
610	34	60.7	842	2	Q5A5U0_CANAL	Q5a5u0 candida alb	683	33	58.9	163	2	Q67JH1_SYMTH	Q67jh1 symbiobacte
611	34	60.7	842	2	Q8NBS1_HUMAN	Q8nbs1 homo sapien	684	33	58.9	164	2	Q9NUW0_HUMAN	Q9nuw0 homo sapien
612	34	60.7	891	2	Q8GHT8_PSERE	Q8ght8 pseudomonas	685	33	58.9	165	2	Q8TY99_METKA	Q8ty99 methanopyru
613	34	60.7	902	2	Q756N1_ASHGO	Q756n1 ashya goss	686	33	58.9	168	2	Q51045_XENLA	Q51045 xenopus lae
614	34	60.7	905	2	Q4RTX3_TETNG	Q4rtx3 tetraodon n	687	33	58.9	169	2	Q5E4B6_VIBF1	Q5e4b6 vibrio floc
615	34	60.7	907	2	Q87W28_PSESM	Q87w28 pseudomonas	688	33	58.9	180	2	Q7Q085_ANOGA	Q7q085 anopheles g

689	33	58.9	183	2	Q9Y9G7_AERPE	Q9Y9G7_aeropyrum p	762	33	58.9	336	2	P71615_MYCTU	P71615_mycobacteri
690	33	58.9	184	2	Q8GMC6_STRLI	Q8Gmc6 streptomyce	763	33	58.9	336	2	Q7TXQ9_MYCBO	Q7txq9 mycobacteri
691	33	58.9	186	2	Q6CRH7_MOUSE	Q6crh7 mus musculu	764	33	58.9	339	2	Q61S15_CABBR	Q61s15 caenorhabdi
692	33	58.9	189	1	QXYR_MYCKE	Q87883 mycobacteri	765	33	58.9	347	2	Q4LQR3_9BURK	Q4lqr3 burkholderi
693	33	58.9	190	2	Q5JWA9_HUMAN	Q5jwa9 homo sapien	766	33	58.9	349	2	Q7WE68_BORBR	Q7we68 bordetella
694	33	58.9	191	1	MOBA_PSEPK	Q8jha3 pseudomonas	767	33	58.9	350	2	Q4LVU3_9URKH	Q4lvu3 burkholderi
695	33	58.9	191	1	MOBA_PSEPU	Q8www0 pseudomonas	768	33	58.9	350	2	Q6TGI4_BRARE	Q6tgi4 brachydanio
696	33	58.9	191	2	Q6IH18_DROME	Q6iha8 drosophila	769	33	58.9	351	2	Q4LM86_9BURK	Q4lm86 burkholderi
697	33	58.9	196	2	Q569A3_RAT	Q569a3 rattus norv	770	33	58.9	352	2	Q81SM8_PLAF7	Q81sm8 plasmodium
698	33	58.9	197	2	Q6NUJ2_HUMAN	Q6nuj2 homo sapien	771	33	58.9	356	2	Q672I3_CHEPO	Q672i3 ctenosacch
699	33	58.9	197	2	Q5RCL0_PONPY	Q5rclo pongo pygma	772	33	58.9	356	2	Q9W7C4_CVPCA	Q9w7c4 cyprinus ca
700	33	58.9	197	2	Q8BGX3_MACFA	Q8bgx9 macaca fasc	773	33	58.9	357	2	SNPC2_MOUSE	SNPC2 mus musculu
701	33	58.9	198	1	MOBA_PSEAB	Q88799 pseudomonas	774	33	58.9	359	1	Q9HTI9_HUMAN	Q9ht19 homo sapien
702	33	58.9	201	1	MOBA_PSEEM	Q88396 pseudomonas	775	33	58.9	376	2	Q8GT57_CUCMA	Q8gt57 cucurbita m
703	33	58.9	202	1	DIPA_HUMAN	Q15834 homo sapien	776	33	58.9	377	2	Q4SJ67_TETNG	Q4sj67 tetraodon n
704	33	58.9	202	1	DIPA_MOUSE	Q6pdy0 mus musculu	777	33	58.9	384	2	Q6L2H1_PICTO	Q6l2h1 picrophilus
705	33	58.9	202	2	Q96HA0_HUMAN	Q96ha0 homo sapien	778	33	58.9	390	2	Q829I6_STRAW	Q829i6 streptomyce
706	33	58.9	202	2	Q5UWA8_HUMAN	Q5uwa8 homo sapien	779	33	58.9	392	2	Q829I6_STRAW	Q829i6 streptomyce
707	33	58.9	208	2	Q5UWA7_HUMAN	Q5jwa7 homo sapien	780	33	58.9	396	2	Q6KE41_SECCR	Q6ke41 secale cere
708	33	58.9	209	2	Q5KB82_CRYNE	Q5kb82 cryptococcu	781	33	58.9	399	2	Q8GVZ4_ORYSA	Q8gvz4 oryza sativ
709	33	58.9	209	2	Q6J9L1_PANTR	Q6j9l1 pan troglod	782	33	58.9	402	2	Q8H0K8_WHEAT	Q8h0k8 triticum ae
710	33	58.9	213	2	Q6WT61_9TREM	Q6wt61 nanophyetus	783	33	58.9	403	2	Q8TWG7_METKA	Q8twg7 methanopyru
711	33	58.9	214	2	Q8CC42_MOUSE	Q8cc42 mus musculu	784	33	58.9	404	2	Q56TK0_HUMAN	Q56tk0 homo sapien
712	33	58.9	224	2	Q55MG0_CRYNE	Q55mg0 cryptococcu	785	33	58.9	405	2	Q5B2Q5_EBENI	Q5b2q5 aspergillus
713	33	58.9	224	2	Q55MN3_CRYNE	Q55mn3 cryptococcu	786	33	58.9	419	2	Q4R641_WACEA	Q4r641 macaca fasc
714	33	58.9	224	2	Q5KB08_CRYNE	Q5kb08 cryptococcu	787	33	58.9	420	1	CI072_MOUSE	CI072 mus musculu
715	33	58.9	224	2	UNG_XYLFA	Q9pa28 xyella fas	788	33	58.9	420	2	Q75866_HUMAN	Q75866 homo sapien
716	33	58.9	253	1	UNG_XYLFA	Q87920 xyella fas	789	33	58.9	421	2	Q8H930_ORYSA	Q8h930 oryza sativ
717	33	58.9	255	2	Q55X09_CRYNE	Q55x09 cryptococcu	790	33	58.9	427	1	GR43A_DROME	GR43a drosophila
718	33	58.9	255	2	Q7NSB3_CHRVO	Q7nsb2 chromobacte	791	33	58.9	427	2	Q5B5S4_EBENI	Q5b5s4 aspergillus
719	33	58.9	257	2	Q7NCX6_GLOVI	Q7ncx6 gloeobacter	792	33	58.9	429	2	Q8WPF5_HUMAN	Q8wpf5 homo sapien
720	33	58.9	262	2	Q53MM1_ORYSA	Q53mm1 oryza sativ	793	33	58.9	431	2	Q4S8V4_TETNG	Q4s8v4 tetraodon n
721	33	58.9	266	2	Q7XB61_ORYSA	Q7xb61 oryza sativ	794	33	58.9	432	2	Q7NZC9_CHRVO	Q7nzc9 chromobacte
722	33	58.9	269	1	SURE_PROMM	Q7v8i0 prochloroco	795	33	58.9	437	2	Q5KNZ1_CRYNE	Q5knz1 cryptococcu
723	33	58.9	270	2	Q5VOL0_ORYSA	Q5vgl0 oryza sativ	796	33	58.9	439	2	Q4V233_DROME	Q4v233 drosophila
724	33	58.9	271	2	Q4HZZ0_GIBZE	Q4hzz0 gibberella	797	33	58.9	441	2	Q4VBZ3_HUMAN	Q4vbz3 homo sapien
725	33	58.9	272	2	Q6YZ19_ORYSA	Q6yz19 oryza sativ	798	33	58.9	444	1	CF8G_CEPAC	CF8g cephalospor
726	33	58.9	274	1	SCF_FELCA	Q79169 felis silve	799	33	58.9	444	2	Q7LLJ3_CEPAC	Q7llj3 cephalospor
727	33	58.9	275	2	Q4WQP3_ASPFU	Q4wqp3 aspergillus	800	33	58.9	444	2	Q4QBU8_LEIMA	Q4qbu8 leishmania
728	33	58.9	279	2	Q726A9_DRSVH	Q726a9 desulfovibr	801	33	58.9	444	2	Q69L18_ORYSA	Q69l18 oryza sativ
729	33	58.9	289	2	Q55LD8_CRYNE	Q55ld8 cryptococcu	802	33	58.9	445	2	Q7ZT39_TETNG	Q7zt39 tetraodon n
730	33	58.9	289	2	Q5KA50_CRYNE	Q5ka50 cryptococcu	803	33	58.9	446	1	SOX8_HUMAN	SOX8 homo sapien
731	33	58.9	290	2	Q7NS16_CHRVO	Q7ns16 chromobacte	804	33	58.9	447	2	Q4SQR1_TETNG	Q4sqr1 tetraodon n
732	33	58.9	291	2	Q7WBF9_BORPA	Q7wbf9 bordetella	805	33	58.9	448	2	Q42907_SCHPO	Q42907 schizosacch
733	33	58.9	291	2	Q7WMY0_BORBR	Q7wmy0 bordetella	806	33	58.9	449	2	Q4SYK8_TETNG	Q4syk8 tetraodon n
734	33	58.9	292	2	Q5VQK9_ORYSA	Q5vqk9 oryza sativ	807	33	58.9	460	2	Q8HKM6_9GOCI	Q8hkm6 eleotris ac
735	33	58.9	294	2	Q9VD42_AERPE	Q9vd42 aeropyrum p	808	33	58.9	460	2	Q8HLR5_ANOCI	Q8hlr5 anoplogaste
736	33	58.9	296	1	FBX37_HUMAN	Q9h469 homo sapien	809	33	58.9	462	2	Q94SQ0_9TELE	Q94sq0 hoplostethu
737	33	58.9	296	1	FBX37_MOUSE	Q91w61 mus musculu	810	33	58.9	462	2	Q6TLH8_BRARE	Q6tlh8 brachydanio
738	33	58.9	298	2	Q4K6W0_PSEF5	Q4k6w0 pseudomonas	811	33	58.9	465	2	Q63K56_BURPS	Q63k56 burkholderi
739	33	58.9	299	2	Q69758_PSEFL	Q69758 pseudomonas	812	33	58.9	465	2	Q4V2Q3_BURMA	Q4v2q3 burkholderi
740	33	58.9	309	2	Q6UPY0_XANCP	Q4upy0 xanthomonas	813	33	58.9	465	2	Q803C9_BRARE	Q803c9 brachydanio
741	33	58.9	309	2	Q8P4C9_XANCP	Q8p4c9 xanthomonas	814	33	58.9	481	1	CI072_HUMAN	CI072 rattus norv
742	33	58.9	311	1	QXYR_MYCAV	P52677 mycobacteri	815	33	58.9	481	1	CI072_RAT	CI072 rattus norv
743	33	58.9	311	1	QXYR_MYCLB	P52678 mycobacteri	816	33	58.9	487	2	Q76DT1_PEA	Q76dt1 pieum sativ
744	33	58.9	311	2	Q5KF45_CRYNE	Q5kf45 cryptococcu	817	33	58.9	488	1	TRI134_HUMAN	TRI134 pieum sativ
745	33	58.9	311	2	Q5JWA5_HUMAN	Q5jwa5 homo sapien	818	33	58.9	488	2	Q54JF6_DICDI	Q54jf6 dictyosteli
746	33	58.9	312	2	Q6ZW94_HUMAN	Q6zw94 homo sapien	819	33	58.9	496	2	Q8XUL0_RALSO	Q8xul0 ralstonia s
747	33	58.9	312	2	Q6GS38_9UROC	Q6gs38 oikopleura	820	33	58.9	498	1	TRI122_HUMAN	TRI122 homo sapien
748	33	58.9	314	2	Q7WMS7_HAEDU	Q7wms7 haemophilus	821	33	58.9	499	2	Q26660_STRPU	Q26660 stronglyloce
749	33	58.9	315	2	Q8PFY9_XANAC	Q8pfy9 xanthomonas	822	33	58.9	505	2	Q6GP18_HUMAN	Q6gp18 homo sapien
750	33	58.9	316	2	Q7D6H2_MYCTU	Q7d6h2 mycobacteri	823	33	58.9	514	2	Q8NHP7_HUMAN	Q8nhp7 homo sapien
751	33	58.9	317	2	Q4V4A1_MYCPA	Q4v4a1 mycobacteri	824	33	58.9	517	2	Q8N644_HUMAN	Q8n644 neurospora
752	33	58.9	317	2	Q8K3B2_MOUSE	Q8k3b2 mus musculu	825	33	58.9	528	2	Q8N644_HUMAN	Q8n644 neurospora
753	33	58.9	317	2	Q4QDS6_RAT	Q4qds6 rattus norv	826	33	58.9	531	2	Q4V7R2_XENLA	Q4v7r2 xenopus lae
754	33	58.9	324	2	Q732L2_MYCPA	Q732l2 mycobacteri	827	33	58.9	534	2	Q5ZE52_ORYSA	Q5ze52 oryza sativ
755	33	58.9	325	2	Q6DEI5_BRARE	Q6dei5 brachydanio	828	33	58.9	536	2	Q51VL8_MAGGR	Q51vl8 magnaporthe
756	33	58.9	326	2	Q6BRJ2_MOUSE	Q6brj2 mus musculu	829	33	58.9	536	2	Q9VC10_DROME	Q9vc10 drosophila
757	33	58.9	327	2	Q7L3C2_HUMAN	Q7l3c2 homo sapien	830	33	58.9	544	2	Q8H2U1_ORYSA	Q8h2u1 oryza sativ
758	33	58.9	329	2	Q83XN5_STRICT	Q83xn5 streptomyce	831	33	58.9	545	2	Q41M96_GIBZE	Q41m96 gibberella
759	33	58.9	329	2	Q80YV0_MOUSE	Q80yv0 mus musculu	832	33	58.9	546	2	Q5FVW8_RAT	Q5fvw8 rattus norv
760	33	58.9	332	2	ARSC_BUCAI	P57156 buchnera ap	833	33	58.9	556	2	Q8QFM3_BRARE	Q8qfm3 brachydanio
761	33	58.9	334	1			834	33	58.9	557	2		

P71615	mycobacteri
P71615	mycobacteri
Q61a15	caenorhabdi
Q41q3	burkholderi
Q7we68	bordetella
Q4lv3	burkholderi
Q6tgi4	brachydanio
Q4lm86	burkholderi
Q81sm8	plasmodium
Q97n6	schizosacch
Q672i3	cyprinophar
Q9w7c4	cyprinus ca
Q91xa5	mus musculu
Q9ht19	homo sapien
Q8gt57	cucurbita m
Q4sj67	tetraodon n
Q6l2h1	picrophilus
Q829i6	streptomyce
Q829i6	streptomyce
Q6ke41	secale cere
Q8gvz4	oryza sativ
Q8h0k8	triticum ae
Q8twg7	methanopyru
Q56tk0	homo sapien
Q5b2q5	aspergillus
Q4r641	macaca fasc
Q6d7u0	mus musculu
Q75866	homo sapien
Q8h930	oryza sativ
Q9v4k2	drosophila
Q5b5e4	aspergillus
Q8wrf5	homo sapien
Q8avf4	tetraodon n
Q7nzc9	chromobacte
Q5kz1	cryptococcu
Q9vz7	drosophila
Q4vzb3	homo sapien
P39058	c acetyl-co
Q7llj3	cephalospor
Q4qb8	leishmania
Q69118	oryza sativ
Q7zt39	tetraodon n
P57073	homo sapien
Q4sq1	tetraodon n
Q42907	schizosacch
Q4syk8	tetraodon n
Q8hk86	eleotris ac
Q8hlr5	anoplোগaste
Q9sq0	hoplostethu
Q6tl8	brachydanio
Q6k56	burkholderi
Q4v3q3	burkholderi
Q803c9	brachydanio
Q961r7	homo sapien
Q66b3	rattus norv
Q66b3	rattus norv
Q7bdt1	pisum sativ
Q9b74	homo sapien
Q54j06	raletostella
Q8x10	dictyonisia
Q8hlr5	homo sapien
Q8lm9	homo sapien
Q26660	strongyloce
Q6gp18	homo sapien
Q8np7	homo sapien
Q7rw94	neurospora
Q8n644	homo sapien
Q4v7r2	xenopus lae
Q5ze52	oryza sativ
P5v18	magnaporthe
Q9vc10	drosophila
Q8m2u1	oryza sativ
Q4lm96	gibberella
Q5fwm8	rattus norv
Q7zu08	brachydanio
Q8qfm3	brachydanio

835	33	58.9	558	2	Q5V5Z0_HUMAN	Q5vaz0 homo sapien	908	33	58.9	1754	2	Q4Q801_LEIMA	Q4q801 leishmania
836	33	58.9	559	2	Q86NK1_DROME	Q86nk1 drosophila	909	33	58.9	1775	1	STRC_HUMAN	Q7rtu9 homo sapien
837	33	58.9	560	2	Q8CDF7_MOUSE	Q8cdf7 mus muscu	910	33	58.9	1918	2	Q84Q97_ORYSA	Q84q97 oryza sativ
838	33	58.9	561	2	Q529R9_MAGGR	Q529r9 magnaporthe	911	33	58.9	1931	1	Q9SFU6_ARATH	Q9sfu6 arabidopsis
839	33	58.9	562	2	Q47U55_TETNG	Q47u55 tetraodon n	912	33	58.9	2006	1	SAYP_DROME	Q9vaf2 drosophila
840	33	58.9	563	2	Q6IKS4_CABER	Q6iks4 caenorhabdi	913	33	58.9	2098	2	Q4WKW9_ASFPF	Q4wkW9 aspergillus
841	33	58.9	564	2	Q9T703_CERSB	Q9t703 ceratophyll	914	33	58.9	3192	2	Q9L4W4_GACTO	Q9l4w4 streptomyce
842	33	58.9	565	2	Q9T704_CERDE	Q9t704 ceratophyll	915	33	58.9	3351	2	Q8IBK4_PLAF7	Q8ibk4 plasmodium
843	33	58.9	566	2	Q8EH13_SHEON	Q8eh13 shewanella	916	32.5	58.0	149	2	Q5YV47_NOCFA	Q5yV47 nocardia fa
844	33	58.9	567	2	Q59GV4_HUMAN	Q59gv4 homo sapien	917	32.5	58.0	323	2	Q4JBZ8_SULAC	Q4jbz8 sulfolobus
845	33	58.9	568	2	Q66659_9GAMA	Q66659 equid herpe	918	32.5	58.0	472	2	Q9SN66_HUMAN	Q9sn66 homo sapien
846	33	58.9	569	2	Q8RIV5_MOUSE	Q8riv5 mus muscu	919	32	57.1	23	2	Q7FD61_ANOGA	Q7fd61 anophetes g
847	33	58.9	570	2	Q5LIQ7_MAGGR	Q5liq7 magnaporthe	920	32	57.1	53	2	Q4Y2F0_PLACH	Q4y2f0 plasmodium
848	33	58.9	571	2	Q5LIQ7_MAGGR	Q5liq7 magnaporthe	921	32	57.1	53	2	Q7UEM5_RHOBA	Q7uem5 rhodopirell
849	33	58.9	572	2	Q5KTP9_OREMO	Q5ktp9 oreochromis	922	32	57.1	58	2	Q5ZB29_ORYSA	Q5zb29 oryza sativ
850	33	58.9	573	2	Q4T820_TETNG	Q4t820 tetraodon n	923	32	57.1	66	2	Q829E4_STRAW	Q829e4 streptomyce
851	33	58.9	574	2	Q4T820_TETNG	Q4t820 tetraodon n	924	32	57.1	69	1	NLTPX_ORYSA	Q83210 oryza sativ
852	33	58.9	575	2	Q4T820_TETNG	Q4t820 tetraodon n	925	32	57.1	70	2	Q716A6_MOUSE	Q716a6 mus muscu
853	33	58.9	576	2	Q7S2T6_NEUCR	Q7s2t6 neurospora	926	32	57.1	72	2	Q8W727_9CAUD	Q8w727 cyanophage
854	33	58.9	577	2	Q917W4_DROME	Q917w4 drosophila	927	32	57.1	74	2	Q6K761_ORYSA	Q6k761 oryza sativ
855	33	58.9	578	2	Q917W4_DROME	Q917w4 drosophila	928	32	57.1	78	2	Q4Z2B2_PLABE	Q4z2b2 plasmodium
856	33	58.9	579	2	Q917W4_DROME	Q917w4 drosophila	929	32	57.1	85	2	Q5BU22_9TRAC	Q5bu22 selaginella
857	33	58.9	580	2	Q917W4_DROME	Q917w4 drosophila	930	32	57.1	87	2	Q5VNY4_ORYSA	Q5vny4 oryza sativ
858	33	58.9	581	2	Q917W4_DROME	Q917w4 drosophila	931	32	57.1	87	2	Q6YVH5_ORYSA	Q6yvH5 oryza sativ
859	33	58.9	582	2	Q917W4_DROME	Q917w4 drosophila	932	32	57.1	87	2	Q6Z196_ORYSA	Q6z196 oryza sativ
860	33	58.9	583	2	Q917W4_DROME	Q917w4 drosophila	933	32	57.1	88	2	Q74DJ1_GEOSL	Q74dj1 geobacter s
861	33	58.9	584	2	Q917W4_DROME	Q917w4 drosophila	934	32	57.1	89	2	Q8K1P6_MOUSE	Q8k1p6 mus muscu
862	33	58.9	585	2	Q917W4_DROME	Q917w4 drosophila	935	32	57.1	91	2	Q5BTA2_SCHJA	Q5bta2 schistosoma
863	33	58.9	586	2	Q917W4_DROME	Q917w4 drosophila	936	32	57.1	91	2	Q7UHB9_RHOBA	Q7uhb9 rhodopirell
864	33	58.9	587	2	Q917W4_DROME	Q917w4 drosophila	937	32	57.1	96	2	Q4O631_ORYSA	Q4o631 oryza sativ
865	33	58.9	588	2	Q917W4_DROME	Q917w4 drosophila	938	32	57.1	102	2	Q6S713_ORYSA	Q6s713 oryza sativ
866	33	58.9	589	2	Q917W4_DROME	Q917w4 drosophila	939	32	57.1	108	2	Q8W332_ORYSA	Q8w332 oryza sativ
867	33	58.9	590	2	Q917W4_DROME	Q917w4 drosophila	940	32	57.1	108	2	Q8BZD5_MOUSE	Q8bzD5 mus muscu
868	33	58.9	591	2	Q917W4_DROME	Q917w4 drosophila	941	32	57.1	115	2	Q5QM55_ORYSA	Q5qm55 oryza sativ
869	33	58.9	592	2	Q917W4_DROME	Q917w4 drosophila	942	32	57.1	124	2	Q4TI00_TETNG	Q4ti00 tetraodon n
870	33	58.9	593	2	Q917W4_DROME	Q917w4 drosophila	943	32	57.1	126	2	Q8FPU2_HUMAN	Q8fpu2 homo sapien
871	33	58.9	594	2	Q917W4_DROME	Q917w4 drosophila	944	32	57.1	141	2	Q57B18_BRUAB	Q57b18 bruceella ab
872	33	58.9	595	2	Q917W4_DROME	Q917w4 drosophila	945	32	57.1	143	2	Q8YJAO_BRUME	Q8yja0 bruceella me
873	33	58.9	596	2	Q917W4_DROME	Q917w4 drosophila	946	32	57.1	143	2	Q6ZP28_HUMAN	Q6zp28 homo sapien
874	33	58.9	597	2	Q917W4_DROME	Q917w4 drosophila	947	32	57.1	143	2	Q6Z330_MOUSE	Q6z330 mus muscu
875	33	58.9	598	2	Q917W4_DROME	Q917w4 drosophila	948	32	57.1	144	2	Q7SV06_ORYSA	Q7sv06 oryza sativ
876	33	58.9	599	2	Q917W4_DROME	Q917w4 drosophila	949	32	57.1	145	2	Q8NBB5_HUMAN	Q8nbb5 homo sapien
877	33	58.9	600	2	Q917W4_DROME	Q917w4 drosophila	950	32	57.1	146	1	DUT_TROW8	Q83122 tropheryma
878	33	58.9	601	2	Q917W4_DROME	Q917w4 drosophila	951	32	57.1	146	1	DUT_TROW8	Q83943 tropheryma
879	33	58.9	602	2	Q917W4_DROME	Q917w4 drosophila	952	32	57.1	149	2	Q5Y4P3_NPVAP	Q5y4p3 antherea p
880	33	58.9	603	2	Q917W4_DROME	Q917w4 drosophila	953	32	57.1	150	2	Q6Z0S9_ORYSA	Q6z0s9 oryza sativ
881	33	58.9	604	2	Q917W4_DROME	Q917w4 drosophila	954	32	57.1	151	2	Q5B4L8_EMENI	Q5b4l8 aspergillus
882	33	58.9	605	2	Q917W4_DROME	Q917w4 drosophila	955	32	57.1	152	2	Q8FYJ8_BRUSU	Q8fyj8 bruceella su
883	33	58.9	606	2	Q917W4_DROME	Q917w4 drosophila	956	32	57.1	154	1	X_HPBVL	P12912 hepatitis b
884	33	58.9	607	2	Q917W4_DROME	Q917w4 drosophila	957	32	57.1	154	2	Q4YGY8_PLABE	Q4ygy8 plasmodium
885	33	58.9	608	2	Q917W4_DROME	Q917w4 drosophila	958	32	57.1	156	2	Q7T5P8_GVCL	Q7t5p8 cryptophleb
886	33	58.9	609	2	Q917W4_DROME	Q917w4 drosophila	959	32	57.1	157	2	Q8N1G8_HUMAN	Q8n1g8 homo sapien
887	33	58.9	610	2	Q917W4_DROME	Q917w4 drosophila	960	32	57.1	160	2	Q825A7_STRAW	Q825a7 streptomyce
888	33	58.9	611	2	Q917W4_DROME	Q917w4 drosophila	961	32	57.1	160	2	Q82FNC_STRAW	Q82fnc streptomyce
889	33	58.9	612	2	Q917W4_DROME	Q917w4 drosophila	962	32	57.1	162	2	Q5NW63_AZOSE	Q5nw63 azoarcus sp
890	33	58.9	613	2	Q917W4_DROME	Q917w4 drosophila	963	32	57.1	165	2	Q8VL06_LACPL	Q8vl06 lactobacill
891	33	58.9	614	2	Q917W4_DROME	Q917w4 drosophila	964	32	57.1	170	2	Q6I549_ORYSA	Q6i549 oryza sativ
892	33	58.9	615	2	Q917W4_DROME	Q917w4 drosophila	965	32	57.1	170	2	Q8B9S1_SHEON	Q8b9s1 shewanella
893	33	58.9	616	2	Q917W4_DROME	Q917w4 drosophila	966	32	57.1	171	2	Q62520_CAEEL	Q62520 caenorhabdi
894	33	58.9	617	2	Q917W4_DROME	Q917w4 drosophila	967	32	57.1	171	2	Q82520_CAEEL	Q82520 caenorhabdi
895	33	58.9	618	2	Q917W4_DROME	Q917w4 drosophila	968	32	57.1	175	2	Q8P1V8_XANAC	Q8p1v8 xanthomonas
896	33	58.9	619	2	Q917W4_DROME	Q917w4 drosophila	969	32	57.1	176	2	Q6ZM62_HUMAN	Q6zm62 homo sapien
897	33	58.9	620	2	Q917W4_DROME	Q917w4 drosophila	970	32	57.1	178	2	Q6K1K3_CABBR	Q6k1k3 caenorhabdi
898	33	58.9	621	2	Q917W4_DROME	Q917w4 drosophila	971	32	57.1	178	2	Q23641_CAEEL	Q23641 caenorhabdi
899	33	58.9	622	2	Q917W4_DROME	Q917w4 drosophila	972	32	57.1	180	2	Q65XR8_ORYSA	Q65xr8 oryza sativ
900	33	58.9	623	2	Q917W4_DROME	Q917w4 drosophila	973	32	57.1	182	1	DYR_DROME	P17119 drosophila
901	33	58.9	624	2	Q917W4_DROME	Q917w4 drosophila	974	32	57.1	184	2	Q5PQ76_XENLA	Q5pq76 xenopus lae
902	33	58.9	625	2	Q917W4_DROME	Q917w4 drosophila	975	32	57.1	185	2	Q9P4W6_YEAST	Q9p4w6 saccharomyc
903	33	58.9	626	2	Q917W4_DROME	Q917w4 drosophila	976	32	57.1	185	2	Q849F8_STRCL	Q849f8 streptomyce
904	33	58.9	627	2	Q917W4_DROME	Q917w4 drosophila	977	32	57.1	185	2	Q6TMM8_STRCL	Q6tmM8 streptomyce
905	33	58.9	628	2	Q917W4_DROME	Q917w4 drosophila	978	32	57.1	185	2	Q9CWZ0_MOUSE	Q9cwz0 mus muscu
906	33	58.9	629	2	Q917W4_DROME	Q917w4 drosophila	979	32	57.1	185	2	Q9JIB0_MOUSE	Q9jib0 mus muscu
907	33	58.9	630	2	Q917W4_DROME	Q917w4 drosophila	980	32	57.1	188	2	Q8MTJ0_HABIE	Q8mtj0 haematobia

981 Q5JKA3 ORYZA 189 2 Q5JKA3 ORYZA
 982 Q4SCR1 TETNG 190 2 Q4SCR1 TETNG
 983 Q83ZE6 XMICO 191 2 Q83ZE6 XMICO
 984 Q87DN6 XYLETT 191 2 Q87DN6 XYLETT
 985 Q7X46 XENLA 192 2 Q7X46 XENLA
 986 Q6P38 HOMO 192 2 Q6P38 HOMO
 987 Q9BV19 HUMAN 199 2 Q9BV19 HUMAN
 988 Q6ZR66 HUMAN 205 2 Q6ZR66 HUMAN
 989 Q8PPQ9 XANAC 207 2 Q8PPQ9 XANAC
 990 Q73JD7 TREDE 208 2 Q73JD7 TREDE
 991 Q5R805 PONPY 209 2 Q5R805 PONPY
 992 Q4RJN9 TETNG 211 2 Q4RJN9 TETNG
 993 Q6ZHB3 ORYZA 216 2 Q6ZHB3 ORYZA
 994 Q93J35 STRCO 221 2 Q93J35 STRCO
 995 Q4VB33 HUMAN 221 2 Q4VB33 HUMAN
 996 Q72322 LISMF 224 2 Q72322 LISMF
 997 Q92EW8 LISIN 224 2 Q92EW8 LISIN
 998 Q8YA47 LISMO 224 2 Q8YA47 LISMO
 999 Q6AJH1 DESPS 229 2 Q6AJH1 DESPS
 1000 Q55D84 DICDI 230 2 Q55D84 DICDI

ALIGNMENTS

RESULT 1
 Q8C2H6 MOUSE PRELIMINARY; PRT; 222 AA.
 AC Q8C2H6
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E43021G10 product:thymidylate synthase, full insert sequence. (Fragment).
 DE Name:lyms;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischnmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA The FANTOM Consortium,
 RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RT Nature 420:563-573(2002).
 RL [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NOD; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Ito M., Kagawa I., Kasukawa T., Kacoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AK088606; BAC40450.1; -; mRNA.
 DR HSRF; P04818; IHW3.
 DR SMR; Q8C2H6; 1-222.
 DR MGI; MGI:98878; Tyms.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMSNTTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMDYLAT SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT NON TER 1
 SQ SEQUENCE 222 AA; 25133 MW; 300157EB7AC78CA5 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred.No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 |||||

DB 98 LMALPPCHAL 107

RESULT 2

Q8C2R3 MOUSE PRELIMINARY; PRT; 222 AA.

AC Q8C2R3; 222 AA.

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:R430004M05 product:thymidylate synthase, full insert sequence. (Fragment).

DE synthase, full insert sequence. (Fragment).

GN Name=Tyms;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.

RT "High-efficiency full-length cDNA cloning."

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Izawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saio T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saio R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleschmann W., Gaasterland T., Glessi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gasteig M., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S., Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RA The FANTOM Consortium,

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kusunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (KISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NOD; TISSUE=Thymus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP.

CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.

CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

DR EMBL; AK088134; BAC40165.1; -; mRNA.

DR HSSP; P45352; 1R7S.

DR SMR; Q8C2R3; 1-222.

DR MGI; MGI:98878; Tyms.

DR GO; GO:0008169; P:methyltransferase activity; IEA.

DR GO; GO:0004799; P:thymidylate synthase activity; IEA.

DR GO; GO:0016740; P:transferase activity; IEA.

DR GO; GO:0006233; P:dTMP biosynthesis; IEA.

DR GO; GO:0009169; P:nucleotide biosynthesis; IEA.

DR InterPro; IPR000398; Thymidylat synth.

DR Pfam; PF00303; Thymidylat synt; 1.

DR PRINTS; PR00108; THYMDSNTHASE.

DR PRODOM; PD001180; Thymidylat synth; 1.

DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.

KW Methyltransferase; Nucleotide biosynthesis; Transferase.

FT NON_TER 1

ST SEQUENCE 222 AA; 25209 MW; 3E8BDBAF742DCC01 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 222;

Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

QY 1 LMALPPCHAL 10

Db 98 LMALPPCHAL 107

RESULT 3

Q8WYK4 HUMAN PRELIMINARY; PRT; 230 AA.

AC Q8WYK4;

DT 01-MAR-2002 (TREMELrel. 20, Created)

DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Thymidylate synthase.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

OC NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22592598; PubMed=12706968; DOI=10.1016/S0304-3835(03)00005-3;

RA Hisatomi H., Tanemura H., Iizuka T., Katsumata K., Nagao K., Sumida H., Udagawa H., Hikiji K.

RT "Differential alternative splicing expressions of thymidylate synthase

RT isoforms.";
 RL Cancer Lett. 193:127-131(2003).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AB077207; BAB83676.1; -; mRNA.
 DR HSSP; P04818; IHVY.
 DR SMR; Q8WK4; 59-230.
 DR Ensembl; ENSG00000176890; Homo sapiens.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth_1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 230 AA; 26140 MW; D09F8316A504A02A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 DB 106 LMALPPCHAL 115

RESULT 4
 ID Q8WK3 HUMAN PRELIMINARY; PRT; 279 AA.
 AC Q8WK3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thymidylate synthase.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=2592598; PubMed=12706968; DOI=10.1016/S0304-3835(03)00005-3;
 RA Hisatomi H., Tanemura H., Iizuka T., Kateumata K., Nagao K.,
 RA Sumida H., Udagawa H., Hikiji K.;
 RT "Differential alternative splicing expressions of thymidylate synthase
 isoforms.";
 RL Cancer Lett. 193:127-131(2003).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AB077208; BAB83677.1; -; mRNA.
 DR HSSP; P04818; IHVY.
 DR SMR; Q8WK3; 26-279.
 DR Ensembl; ENSG00000176890; Homo sapiens.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth_1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 SQ SEQUENCE 279 AA; 31758 MW; 1083A53DE10AB763 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 DB 155 LMALPPCHAL 164

RESULT 5

TYSY_MOUSE
 ID TYSY_MOUSE STANDARD; PRT; 307 AA.
 AC P07607;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (Tsase).
 GN Name=Tyms;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=88174353; PubMed=3444407;
 RA Perryman S.M., Rossana C., Deng T., Vanin E.F., Johnson L.F.;
 RT "Sequence of a cDNA for mouse thymidylate synthase reveals striking
 similarity with the prokaryotic enzyme.";
 RL Mol. Biol. Evol. 3:313-321(1986).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=87057259; PubMed=3782103;
 RA Deng T., Li D., Jenh C.-H., Johnson L.F.;
 RT "Structure of the gene for mouse thymidylate synthase. Locations of
 introns and multiple transcriptional start sites.";
 RL J. Biol. Chem. 261:16000-16005(1986).
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=89128436; PubMed=2915925;
 RA Deng T., Li Y., Johnson L.F.;
 RT "Thymidylate synthase gene expression is stimulated by some (but not
 all) introns.";
 RL Nucleic Acids Res. 17:645-658(1989).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 DR EMBL; M13019; AAA40439.1; -; mRNA.
 DR EMBL; M13352; AAA40444.1; -; Genomic DNA.
 DR EMBL; J02617; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; M13347; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; M13348; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; M13349; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; M13350; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; M13351; AAA40444.1; JOINED; Genomic DNA.
 DR EMBL; X14489; CAA32651.1; -; mRNA.
 DR PIR; A26323; YXMSY.
 DR HSSP; P45352; IRTS.
 DR SMR; P07607; 21-301.
 DR Ensembl; ENSMUSG00000025747; Mus musculus.
 DR MGI; MGI:98878; Tyms.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth_1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 ACT_SITE 189 By similarity.
 ACT_SITE 189

SQ SEQUENCE 307 AA; 34958 MW; E4930618C487FD5E CRC64;
 Query Match 100.0%; Score 56; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 183 LMALPPCHAL 192
 RESULT 6
 TYSY RAT
 ID TYSY RAT STANDARD; PRT; 307 AA.
 AC P45352;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=Tyms;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95226450; PubMed=7711067; DOI=10.1016/0167-4781(95)00008-5;
 RA Ciesla J., Weiner K.X., Weiner R.S., Reston J.T., Maley G.F.,
 MAley F.;
 RT "Isolation and expression of rat thymidylate synthase cDNA:
 phylogenetic comparison with human and mouse thymidylate synthases.";
 RL Biochim. Biophys. Acta 1261:233-242(1995).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
 RX MEDLINE=99110611; PubMed=9894005; DOI=10.1021/bi981881d;
 RA Sotelo-Mundo R.R., Ciesla J., Dziak J.M., Rode W., Maley F.,
 MAley G.F., Hardy L.W., Montfort W.R.;
 RT "Crystal structures of rat thymidylate synthase inhibited by Tomudex,
 a potent anticancer drug.";
 RL Biochemistry 38:1087-1094(1999).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
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 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC
 DR EMBL; L12138; AA92340.1; -; mRNA.
 DR PIR; S53715;
 DR PDB; 1RTS; X-ray; A/B=1-307.
 DR PDB; 2TSR; X-ray; A/B/C/D=1-307.
 DR RGD; 3921; Tyms.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR Pfam; PF00303; Thymidylat_synth; 1.
 DR PRINTS; PR00108; THYMSNTTHASE.
 DR PRODOM; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMYDLATE SYNTHASE; 1.
 KW 3D-structure; Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT ACT_SITE 189 189 By similarity.
 FT TURN 23 23
 FT HELIX 24 37
 FT STRAND 39 41
 FT STRAND 49 60
 FT STRAND 62 63
 FT TURN 75 86
 FT HELIX 87 88
 FT TURN 91 91
 FT STRAND

FT TURN 92 92
 FT HELIX 93 96
 FT TURN 97 99
 FT TURN 102 104
 FT HELIX 105 107
 FT HELIX 109 114
 FT TURN 115 116
 FT TURN 122 123
 FT TURN 124 124
 FT STRAND 129 134
 FT STRAND 136 136
 FT TURN 137 137
 FT TURN 143 144
 FT TURN 148 149
 FT STRAND 152 152
 FT STRAND 154 164
 FT TURN 166 167
 FT STRAND 172 174
 FT TURN 178 180
 FT HELIX 181 183
 FT STRAND 190 198
 FT TURN 199 200
 FT STRAND 201 212
 FT TURN 213 215
 FT HELIX 216 235
 FT TURN 236 236
 FT STRAND 238 252
 FT HELIX 253 255
 FT STRAND 256 264
 FT STRAND 272 275
 FT HELIX 282 284
 FT HELIX 287 289
 FT STRAND 290 293
 SQ SEQUENCE 307 AA; 35017 MW; 159F564D347B2B52 CRC64;
 Query Match 100.0%; Score 56; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 183 LMALPPCHAL 192
 RESULT 7
 Q544L2 MOUSE PRELIMINARY; PRT; 307 AA.
 AC Q544L2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Adult male urinary bladder cDNA, RIKEN full-length enriched library,
 clone:9530083D17 product:thymidylate synthase, full insert
 DE sequence...
 DE Name=Tyms;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=93279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verdano R., Wagner L., Wang L., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaenuehi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayaseu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muraatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsushita S., Kawai J.,
RA Okazaki Y., Muraatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayaseu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muraatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -I- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -I- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AK035663; BAC29144.1; -; mRNA.
DR MGI; MGI:98878; Tyme.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34958 MW; E4930618C487FDE5 CRC64;
Query Match 100.0%; Score 56; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 183 LMALPPCHAL 192
RESULT 8
Q8VDV6_MOUSE PRELIMINARY; PRT; 307 AA.
ID Q8VDV6_MOUSE
AC Q8VDV6_MOUSE
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tyme protein.
GN Name=tyme;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
[2]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC
CC
CC -|- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -|- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; BC020139; AH020139.1; -; mRNA.
DR HSSP; P45352; IRTS.
DR SNR; Q8VDV6; 21-301.
DR MGI; MGI:98878; Tyms.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synt; 1.
DR PRINTS; PR00108; THYMSNTFAS.
DR ProDom; PD001180; THYMSNTFAS.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;

Query Match 100.0%; Score 56; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
Db 183 LMALPPCHAL 192
|||||||
|||

RESULT 9
ID Q9DOH1_MOUSE
AC Q9DOH1_MOUSE PRELIMINARY; PRT; 307 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610017621 product:thymidylate synthase, full
DE insert sequence.
DE
DE Name=Tyms;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
CC "High-efficiency full-length cDNA cloning.";
CC Meth. Enzymol. 303:19-44 (1999).
CC [2]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojorori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
[2]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC
CC
CC -|- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -|- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; BC020139; AH020139.1; -; mRNA.
DR HSSP; P45352; IRTS.
DR SNR; Q8VDV6; 21-301.
DR MGI; MGI:98878; Tyms.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synt; 1.
DR PRINTS; PR00108; THYMSNTFAS.
DR ProDom; PD001180; THYMSNTFAS.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;

Query Match 100.0%; Score 56; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
Db 183 LMALPPCHAL 192
|||||||
|||

RESULT 9
ID Q9DOH1_MOUSE
AC Q9DOH1_MOUSE PRELIMINARY; PRT; 307 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610017621 product:thymidylate synthase, full
DE insert sequence.
DE
DE Name=Tyms;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
CC "High-efficiency full-length cDNA cloning.";
CC Meth. Enzymol. 303:19-44 (1999).
CC [2]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA Saito T., Okazaki Y., Gojorori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
[2]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC
CC
CC -|- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -|- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; BC020139; AH020139.1; -; mRNA.
DR HSSP; P45352; IRTS.
DR SNR; Q8VDV6; 21-301.
DR MGI; MGI:98878; Tyms.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synt; 1.
DR PRINTS; PR00108; THYMSNTFAS.
DR ProDom; PD001180; THYMSNTFAS.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 34930 MW; 76F797162468FD9D CRC64;

Query Match 100.0%; Score 56; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
Db 183 LMALPPCHAL 192
|||||||
|||

RESULT 9
ID Q9DOH1_MOUSE
AC Q9DOH1_MOUSE PRELIMINARY; PRT; 307 AA.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610017621 product:thymidylate synthase, full
DE insert sequence.
DE
DE Name=Tyms;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RT NUCLEOTIDE SEQUENCE.
RN STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)

DR PRINTS; PR00108; THYMDSNTNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 307 AA; 34989 MW; E493061852CE7EE CRC64;
 Query Match 100.0%; Score 56; DB 2; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LMALPPCHAL 10
 Db 183 LMALPPCHAL 192
 RESULT 10
 TSY_HUMAN STANDARD; PRT; 312 AA.
 AC F04818;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=TYMS; Synonyms=TS; ORFNames=OK/SW-cl.29;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=85215597; PubMed=2987839;
 RX Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;
 RA "Nucleotide sequence of a functional cDNA for human thymidylate
 RT synthase";
 RL Nucleic Acids Res. 13:2035-2043(1985).
 RN [2]
 RP MEDLINE=91056070; PubMed=2243092;
 RX Kaneda S., Nalbantoglu J., Takeishi K., Shimizu K., Gotoh O., Seno T.,
 RA Ayusawa D.;
 RT "Structural and functional analysis of the human thymidylate synthase
 RT gene";
 RL J. Biol. Chem. 265:20277-20284(1990).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Colon adenocarcinoma;
 RA Shichijo S., Itoh K.;
 RT "Identification of immuno-peptidomics that are recognized by tumor-
 RT reactive CTL generated from TIL of colon cancer patients.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Bone marrow, Placenta, and Skin;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 1-67.
 RX MEDLINE=90110051; PubMed=2532645;
 RA Takeishi K., Kaneda S., Ayusawa D., Shimizu K., Gotoh O., Seno T.;
 RT "Human thymidylate synthase gene: isolation of phage clones which
 RT cover a functionally active gene and structural analysis of the region
 RT upstream from the translation initiation codon."; J. Biochem. 106:575-583(1989).
 RN [6]
 RP PROTEIN SEQUENCE OF 1-24.
 RX MEDLINE=85261174; PubMed=3839505;
 RA Shimizu K., Ayusawa D., Takeishi K., Seno T.;
 RT "Purification and NH2-terminal amino acid sequence of human
 RT thymidylate synthase in an overproducing transformant of mouse FM3A
 RT cells."; J. Biochem. 97:845-850(1985).
 RN [7]
 RP PROTEIN SEQUENCE OF 1-9.
 RX MEDLINE=89255401; PubMed=2656695;
 RA Davissou V.J., Sirawaporn W., Santi D.V.;
 RT "Expression of human thymidylate synthase in Escherichia coli."; J. Biol. Chem. 264:9145-9148(1989).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=96110704; PubMed=8845352;
 RA Schiffer C.A., Clifton I.J., Davissou V.J., Santi D.V., Stroud R.M.;
 RT "Crystal structure of human thymidylate synthase: a structural
 RT mechanism for guiding substrates into the active site."; Biochemistry 34:16279-16287(1995).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=21229106; PubMed=11329255; DOI=10.1021/bi002413i;
 RA Phan J., Koli S., Minor W., Dunlap R.B., Berger S.H., Lebioda L.;
 RT "Human thymidylate synthase is in the closed conformation when
 RT complexed with dUMP and raltitrexed, an antifolate drug."; Biochemistry 40:1897-1902(2001).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=2126721; PubMed=11278511; DOI=10.1074/jbc.M009493200;
 RA Phan J., Steadman D.J., Koli S., Ding W.C., Minor W., Dunlap R.B.,
 RA Berger S.H., Lebioda L.;
 RT "Structure of human thymidylate synthase suggests advantages of
 RT chemotherapy with noncompetitive inhibitors."; J. Biol. Chem. 276:14170-14177(2001).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; X02308; CAA26178.1; -; mRNA.
 DR EMBL; D00596; BAA00472.1; -; Genomic_DNA.
 DR EMBL; AB062290; BAB93473.1; -; mRNA.
 DR EMBL; BC002567; AAH02567.1; -; mRNA.
 DR EMBL; BC013919; AAH13919.1; -; mRNA.
 DR EMBL; BC083512; AAH83512.1; -; mRNA.
 DR EMBL; D00517; BAA00404.1; -; Genomic_DNA.
 DR PIR; A23047; YXHUT.
 DR PDB; 1HVY; X-ray; A/B/C/D=25-312.
 DR PDB; 1HW3; X-ray; A=1-312.
 DR PDB; 1HW4; X-ray; A=1-312.
 DR PDB; 1HZW; X-ray; A/B=29-312.
 DR PDB; 1I00; X-ray; A/B=29-312.
 DR PDB; 1J06; X-ray; A/B/C/D=1-312.
 DR PDB; 1J07; X-ray; A/B/C/D=1-312.
 DR PDB; 1J08; X-ray; A/B/C/D=1-312.

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DR Ensembl; ENSG00000176890; Homo sapiens.
DR HGNC; HGNC:12441; TYMS.
DR H-InvDB; HIX0017793; -.
DR Reactome; R04818; -.
DR MIM; 188350; -.
DR GO; GO:0009157; P:deoxyribonucleoside monophosphate biosynthesis; TAS.
DR GO; GO:0006281; P:DNA repair; NAS.
DR GO; GO:0006260; P:DNA replication; NAS.
DR GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . . ; TAS.
DR GO; GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR InterPro; IPR000398; Thymidylat_synth.
DR Pfam; PF00303; Thymidylat_synth; 1.
DR PRINTS; PR00108; THYMDSNTASE.
DR ProDom; PD001180; THYMIDYLAT_SYNTHASE; 1.
DR 3D-structure; Direct protein sequencing; Methyltransferase;
KW Nucleotide biosynthesis; transferase.
FT INIT MET 0 0
FT ACT SITE 194 194
FT TURN 28 28
FT HELIX 29 42
FT STRAND 44 46
FT TURN 49 50
FT STRAND 54 65
FT TURN 67 68
FT TURN 74 77
FT HELIX 80 91
FT TURN 92 93
FT STRAND 96 96
FT HELIX 97 101
FT TURN 102 104
FT TURN 107 109
FT HELIX 110 112
FT HELIX 114 119
FT TURN 120 121
FT TURN 123 124
FT TURN 127 128
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FT HELIX 134 140
FT STRAND 141 141
FT TURN 142 142
FT TURN 148 149
FT TURN 153 154
FT STRAND 157 157
FT HELIX 159 169
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FT STRAND 206 217
FT TURN 218 220
FT TURN 221 239
FT STRAND 243 257
FT HELIX 258 260
FT HELIX 261 268
FT TURN 269 269
FT STRAND 277 280
FT HELIX 287 289
FT HELIX 292 294
FT STRAND 295 298
SQ SEQUENCE 312 AA; 35585 MW; A66F0B6D1973AB41 CRC64;

Query Match 100.0%; Score 56; DB 1; Length 312;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 188 LMALPPCHAL 197
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RESULT 11
Q53FB7 HUMAN
ID Q53FB7 HUMAN PRELIMINARY; PRT; 313 AA.
AC Q53FB7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Thymidylate synthetase variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AK223372; BAD97092.1; -; mRNA.
DR GO; GO:0004799; P:thymidylate synthase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
FT NON_TER 1
FT SEQUENCE 313 AA; 35717 MW; 4B8797D5133B5B67 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198
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RESULT 12
Q53Y97 HUMAN
ID Q53Y97 HUMAN PRELIMINARY; PRT; 313 AA.
AC Q53Y97;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Thymidylate synthetase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
```

RT vector.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; BT006811; AAP3457.1; -; mRNA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 313 AA; 35716 MW; 148D377F19915B6A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 |||||
 DB 189 LMALPPCHAL 198

RESULT 13

Q6P045 BRARE PRELIMINARY; PRT; 318 AA.
 AC Q6P045;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Tyms protein.
 GN Name=tyms;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RG NIH MGC Project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; BC065845; AAH5845.1; -; mRNA.
 DR HSSP; P00470; 1AXW.
 DR ZFIN; ZDB-GENE-040426-59; tyms.
 DR GO; GO:0004799; F:methyltransferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMSDNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYIMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 318 AA; 36183 MW; 47E9BABA24927372 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 318;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 |||||
 DB 194 LMALPPCHAL 203

RESULT 14

Q7ZUI7 BRARE PRELIMINARY; PRT; 319 AA.
 AC Q7ZUI7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tyms protein.
 GN Name=tyms;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RG NIH MGC Project;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; BC049026; AAH49026.1; -; mRNA.
 DR HSSP; P04818; 1HW4.
 DR ZFIN; ZDB-GENE-040426-59; tyms.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.

DR GO: 0006231; P: dTMP biosynthesis; IEA.
 DR GO: 0009165; P: nucleotide biosynthesis; IEA.
 DR InterPro: IPR000398; Thymidylat synth.
 DR Pfam: PF00303; Thymidylat synt; 1.
 DR PRINTS: PR00108; THYMDSNTHASE.
 DR ProDom: PD001180; Thymidylat synth; 1.
 DR PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 319 AA; 36299 MW; ADFA451E1DDF891A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 DB 195 LMALPPCHAL 204
 |||||

RESULT 15

ID Q9DGH5 BRARE PRELIMINARY; PRT; 319 AA.
 AC Q9DGH5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thymidylate synthase.
 OS Name=tyms; ORFNames=29c:56465; (Danio rerio).
 OS Brachydanio rerio (Zebrafish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RX NCBI_TaxID=7955;
 RV [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gill R.L. Jr., Warren J.T. Jr.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AY005804; AAF97476.1; -; mRNA.
 DR FFIN; ZDB-GENE-040426-59; tyms.
 DR ZFIN; ZDB-GENE-040426-59; tyms.
 DR GO: 0008168; P: methyltransferase activity; IEA.
 DR GO: 0004799; F: thymidylate synthase activity; IEA.
 DR GO: 0016740; F: transferase activity; IEA.
 DR GO: 0006231; P: dTMP biosynthesis; IEA.
 DR GO: 0009165; P: nucleotide biosynthesis; IEA.
 DR InterPro: IPR000398; Thymidylat synth.
 DR Pfam: PF00303; Thymidylat synt; 1.
 DR PRINTS: PR00108; THYMDSNTHASE.
 DR ProDom: PD001180; Thymidylat synth; 1.
 DR PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 SQ SEQUENCE 319 AA; 36313 MW; E08B155B09DE1884 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 319;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 DB 195 LMALPPCHAL 204
 |||||

RESULT 16

ID TVSY_AZOSE STANDARD; PRT; 264 AA.
 AC Q5P233;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA; OrderedLocusNames=AZOSEA25060; ORFNames=eba4415;
 OS Azorarcus sp. (strain EbN1).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
 OC Rhodocyclaceae; Azorarcus.
 OX NCBI_TaxID=76114;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;
 RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F.,
 RA Reinhardt R.;
 RT "The genome sequence of an anaerobic aromatic-degrading denitrifying
 bacterium, strain EbN1.";
 RL Arch. Microbiol. 183:27-36(2005).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 CC biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC
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 CC removed.
 CC
 CC EMBL; CR555306; CAI08631.1; -; Genomic_DNA.
 DR SMR; Q5P233; 1-264.
 DR HAMAP; MF_00008; -; 1.
 DR InterPro: IPR000398; Thymidylat synth.
 DR Pfam: PF00303; Thymidylat synt; 1.
 DR PRINTS: PR00108; THYMDSNTHASE.
 DR ProDom: PD001180; Thymidylat synth; 1.
 DR PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT_SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 30134 MW; CA9BC0C1PAE0629E CRC64;

Query Match 92.9%; Score 52; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 DB 141 MALPPCHAL 149
 |||||

RESULT 17

ID TVSY_NEIMA STANDARD; PRT; 264 AA.
 AC Q9JTS7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA; OrderedLocusNames=NWA1963;
 OS Neisseria meningitidis (serogroup A).....
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
 RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

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RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL meningitidis 22491."
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL162757; CAB85183.1; -; Genomic_DNA.
CC DR PIR; A81825; A81825.
CC DR HSSP; P00470; 1TRG.
CC DR SMR; Q9J757; 1-264.
CC HAMAP; MF_00008; -; 1.
CC InterPro; IPR000398; Thymidylat_synth.
CC Pfam; PF00303; Thymidylat synt; 1.
CC PRINTS; PR00108; THYMSNTHASE.
CC PRODOM; PD001180; Thymidylat synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transferase.
FT ACT SITE 146 146 By similarity.
SQ SEQUENCE 264 AA; 30261 MW; 001E15B55FE16BFC CRC64;

Query Match 92.9%; Score 52; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 2 MALPPCHAL 10
DB 141 MALPPCHAL 149
|||||

RESULT 18
TYSY_NEIMB
ID_TYSY_NEIMB STANDARD; PRT; 264 AA.
AC Q9J72.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thyA; OrderedLocNames=NM1709;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cifton H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Masiagnani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA

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CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE002098; AAF42056.1; -; Genomic_DNA.
CC DR PIR; G81050; G81050.
CC DR HSSP; P00470; 1TRG.
CC DR SMR; Q9J772; 1-264.
CC TIGR; NMB1709; -.
CC HAMAP; MF_00008; -; 1.
CC InterPro; IPR000398; Thymidylat_synth.
CC Pfam; PF00303; Thymidylat synt; 1.
CC PRINTS; PR00108; THYMSNTHASE.
CC PRODOM; PD001180; Thymidylat synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transferase.
FT ACT SITE 146 146 By similarity.
SQ SEQUENCE 264 AA; 30277 MW; 012C15B55FE16BE2 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 264;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 2 MALPPCHAL 10
DB 141 MALPPCHAL 149
|||||

RESULT 19
TYSY_PSEAE
ID_TYSY_PSEAE STANDARD; PRT; 264 AA.
AC Q916F1.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thyA; OrderedLocNames=PA0342;
OS Pseudomonas aeruginosa
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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CC EMBL; AE004472; AAC03731.1; -; Genomic_DNA.
 CC PIR; D83602; D83602.
 CC HSP; P00470; 1TRG.

DR HAMAP; MF 00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth; 1.
 DR PRINTS; PD00108; THYDMSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYDYLAT SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase. 146 146 By similarity.
 FT ACT_SITE 264 AA; 30016 MW; D34075691D06F352 CRC64;
 SQ SEQUENCE 264 AA; 30016 MW; D34075691D06F352 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 DB 141 MALPPCHAL 149

RESULT 20
 ID Q5F732 NEIG1 PRELIMINARY; PRT; 264 AA.
 AC Q5F732
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DE Putative thymidylate synthase B (EC 2.1.1.45).
 GN OrderedLocNames=NG01357;
 OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 CC Neisseriaceae; Neisseria.
 CC NCBI_TaxID=242231;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Lewis L.A., Gillaeay A.F., McLaughlin R.E., Gibson M., Ducey T.F.,
 RA Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
 RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
 RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
 RT "The complete genome sequence of Neisseria gonorrhoeae."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

DR EMBL; AE004969; AAW90005.1; -; Genomic_DNA.
 DR SMR; Q5F732; 1-264.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
 DR InterPro; IPR00398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth; 1.
 DR PRINTS; PD00108; THYDMSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYDYLAT SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 SQ SEQUENCE 264 AA; 30247 MW; 52A71581DD479781 CRC64;

Query Match 92.9%; Score 52; DB 2; Length 264;
 Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 DB 141 MALPPCHAL 149

RESULT 21
 ID TSY NEIGO STANDARD; PRT; 265 AA.
 AC Q3380;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA;
 OS Neisseria gonorrhoeae.
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 CC Neisseriaceae; Neisseria.
 CC NCBI_TaxID=485;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=MS11;
 RX MEDLINE=97372537; PubMed=9228757; DOI=10.1016/S0378-1097(97)00164-X;
 RA Carlson J.H., Hill S.A.;
 RT "Identification and characterization of thymidylate synthase from
 RT Neisseria gonorrhoeae."
 RL FEMS Microbiol. Lett. 151:225-230(1997).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 CC biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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 CC EMBL; U86637; AAC45469.1; ALT_INIT; Genomic_DNA.
 CC HSP; P00470; 1TRG.
 CC SMR; Q3380; 1-265.
 CC HAMAP; MF 00008; -; 1.
 CC InterPro; IPR000398; Thymidylat synth.
 CC Pfam; PF00303; Thymidylat synth; 1.
 CC PRINTS; PD00108; THYDMSNTHASE.
 CC ProDom; PD001180; Thymidylat synth; 1.
 CC PROSITE; PS00091; THYDYLAT SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT ACT_SITE 147 147 By similarity.
 SQ SEQUENCE 265 AA; 30306 MW; 135961EEFAFA3FF8 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 265;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 DB 142 MALPPCHAL 150

RESULT 22
 ID TSY BIFLO STANDARD; PRT; 266 AA.
 AC Q8G3T9;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).

```

GN Name=thyA; OrderedLocusNames=BL1665;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen R.-C., Desiere F., Bork P., Delley M.,
RA Fridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; AE014295; AAN25452.1; -; Genomic_DNA.
CC HSSP; P00470; 1F4F.
CC HAMAP; MF_00008; -; 1.
CC InterPro: IPR000398; Thymidylat synth.
CC Pfam; PF00303; Thymidylat synth_1.
CC PRINTS; PR00108; THYMSNTTHASE.
CC ProDom; PD001180; Thymidylat synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transferase. 149 149 By similarity.
FT ACT_SITE 149 149
SQ SEQUENCE 266 AA; 30689 MW; E8BDC2C48B9DE70 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 144 MALPPCHAL 152
|||||

RESULT 23
Q91CH7_9ALPH PRELIMINARY; PRT; 316 AA.
AC Q91CH7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Thymidylate synthase.
OS Macropodid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=137443;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Giuliani S., Smith G.A., Polkinghorne I., Mahony T.J., Young P.,
RA Mattick J.S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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DR EMBL; AF188480; AAL14421.1; -; Genomic_DNA.
DR HSSP; P04818; 1HZW.
DR SMR; Q91CH7; 30-316.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synth; 1.
DR PRINTS; PR00108; THYMSNTTHASE.
DR ProDom; PD001180; Thymidylat synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 316 AA; 35951 MW; 6241CD877DA4AD0B CRC64;

Query Match 92.9%; Score 52; DB 2; Length 316;
Best Local Similarity 90.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 192 LMALPPCHTL 201
|||||

RESULT 24
Q9E202_9ALPH PRELIMINARY; PRT; 295 AA.
AC Q9E202;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
OS Cercopithecine herpesvirus 9 (Simian varicella virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21251382; PubMed=11352673; DOI=10.1006/viro.2001.0912;
RA Gray W.L., Starnes B., White M.W., Mahalingam R.;
RT "The DNA sequence of the simian varicella virus genome.";
RL Virology 284:123-130 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete sequence of the Simian Varicella Virus Genome.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AF275348; AAG27186.1; -; Genomic_DNA.
DR HSSP; P04818; 1HZW.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synth; 1.
DR PRINTS; PR00108; THYMSNTTHASE.
DR ProDom; PD001180; Thymidylat synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
SQ SEQUENCE 295 AA; 33932 MW; 0AA7C4682DE82838 CRC64;

Query Match 91.1%; Score 51; DB 2; Length 295;
Best Local Similarity 90.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
|||||

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Db 171 LMALPPCHML 180

RESULT 25
 TYSY_HV8
 AC P90463; STANDARD; PRT; 337 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=70;
 OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=37296;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
 RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
 RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
 (HHV8).";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97296220; PubMed=9151804;
 RA Neipel P., Albrecht J.-C., Fleckenstein B.;
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
 human herpesvirus 8: determinants of its pathogenicity?";
 RL J. Virol. 71:4187-4192(1997).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U75698; AAC57092.1; -; Genomic DNA.
 DR EMBL; U83348; AAC56948.1; -; Genomic DNA.
 DR EMBL; U93872; AAB62673.1; -; Genomic DNA.
 DR EMBL; U71365; AAC34940.1; -; Genomic DNA.
 DR HSSP; P04818; LHW4.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Methyltransferase; Nucleotide biosynthesis; Transferase.
 FT ACT SITE 219 219 By similarity.
 SQ SEQUENCE 337 AA; 38555 MW; D0B0CE60A3384EC CRC64;
 Query Match 91.1%; Score 51; DB 1; Length 337;
 Best Local Similarity 90.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 213 LMALPPCHLL 222

RESULT 26
 TYSY_CHV8
 ID TYSY_CHV8 STANDARD; PRT; 264 AA.
 AC Q7NZ95;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA; OrderedLocusNames=CV1027;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Faicao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisaard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leol L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manlio G.P., Maranhao A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.P., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa P.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
 CC -1- FUNCTION: Provides the sole de novo source of dTMP for DNA
 CC biosynthesis (By similarity).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -1- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thymidylate synthase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; AE016913; AAQ59702.1; -; Genomic DNA.
 DR HSSP; P00470; IAXW.
 DR HAMAP; MF_00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 30154 MW; 65FA6807EDB0D42E CRC64;
 Query Match 87.5%; Score 49; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 2.1;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 Db 141 MALPPCHSL 149

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RESULT 27
TYSY_LISIN
ID_TYSY_LISIN STANDARD; PRT; 314 AA.
AC Q92AD4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thyA; OrderedLocusNames=lin1988;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAINS=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
BA Quarero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefz J., Kuhn M., Kust P., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Coseart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL596170; CAC97218.1; -; Genomic_DNA.
CC PIR; A81681.
CC HSP; P00469; ITSY.
CC Listlist; LIN01988; -.
CC HAMAP; MF_00008; -; 1.
CC InterPro; IPR000398; Thymidylat synth.
CC Pfam; PF00303; Thymidylat synt; 1.
CC PRINTS; PR00108; THYMDSNTSHASE.
CC ProDom; PD001180; Thymidylat synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferase.
CC ACT_SITE 196 196 By similarity.
CC SEQUENCE 314 AA; 36146 MW; 33BCC6C461EE674B CRC64;

Query Match 87.5%; Score 49; DB 1; Length 314;
Best Local Similarity 88.9%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
Db 191 MALPPCHSL 199
|||||:|

RESULT 28
TYSY_LISMF
ID_TYSY_LISMF STANDARD; PRT; 314 AA.

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AC Q71YE1;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thyA; OrderedLocusNames=LMOF2365 1904;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.P., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raeko D.A., Anguio S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
RA Bayles D.O., Luchanek J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017328; AAT04673.1; -; Genomic_DNA.
CC HSP; P00470; IAXW.
CC TIGR; LMOF2365 1904; -.
CC HAMAP; MF_00008; -; 1.
CC InterPro; IPR000398; Thymidylat synth.
CC Pfam; PF00303; Thymidylat synt; 1.
CC PRINTS; PR00108; THYMDSNTSHASE.
CC ProDom; PD001180; Thymidylat synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferase.
CC ACT_SITE 196 196 By similarity.
CC SEQUENCE 314 AA; 36177 MW; 7E211F3776F542BE CRC64;

Query Match 87.5%; Score 49; DB 1; Length 314;
Best Local Similarity 88.9%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
Db 191 MALPPCHSL 199
|||||:|

RESULT 29
TYSY_LISMO
ID_TYSY_LISMO STANDARD; PRT; 314 AA.
AC Q8Y626;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thyA; OrderedLocusNames=lmo1874;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

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OX NCBI_TaxID=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glauber P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Chabot A., Berche P., Bloeker H., Brand P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapakt G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voes H., Wehland J., Cossart P.;
RT "Comparative Genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC
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CC removed.
CC
CC EMBL: AL591981; CAC9952.1; -; Genomic_DNA.
DR PIR: AB1309; AB1309.
DR HSP: P00469; ITST.
DR Listlist; LM001874; -.
DR HAMAP; MF_00008; -.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synth; 1.
DR PRINTS; PR00108; THYMDSNTHASE.
DR ProDom; PD001180; THYMIDYLAT_SYNTH; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
DR Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transference.
FT ACT SITE 196 196 By similarity.
FT ACT SITE 314 AA; 36163 MW; 288191ABD21ADF15 CRC64;
SQ SEQUENCE 314 AA; 36163 MW; 288191ABD21ADF15 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 314;
Best Local Similarity 88.9%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 191 MALPPCHSL 199

RESULT 30
Q7T4R2 9GAMA
ID Q7T4R2_9GAMA PRELIMINARY; PRT; 63 AA.
AC Q7T4R2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thymidylate synthase (Fragment).
OS Baboon gamma-herpesvirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=169974;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PaPrV2;
RX MEDLINE=22713713; PubMed=12829855;

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RX DOI=10.1128/JVI.77.14.8159-8165.2003;
RA Whitby D., Stosel A., Gamache C., Papin J., Bosch M., Smith A.,
RA Kedes D.H., White G., Kennedy R., Dittmer D.P.;
RT "Novel Kaposi's sarcoma-associated herpesvirus homolog in baboons.";
RL J. Virol. 77:8159-8165(2003).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AV270027; AAP42245.1; -; Genomic_DNA.
DR HSP; P04818; IHYV.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synth; 1.
DR PRINTS; PR00108; THYMDSNTHASE.
DR ProDom; PD001180; THYMIDYLAT SYNTHASE; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Methyltransferase; Nucleotide biosynthesis; Transferase.
FT NON_TER 1 63
FT NON_TER 63
SQ SEQUENCE 63 AA; 7188 MW; 9EDB4FC6C2C33DD1 CRC64;

Query Match 85.7%; Score 48; DB 2; Length 63;
Best Local Similarity 88.9%; Pred. No. 0.77;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 47 MALPPCHVL 55

RESULT 31
Q8QY23 RTRV
ID Q8QY23_RTRV PRELIMINARY; PRT; 124 AA.
AC Q8QY23;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thymidylate synthase-like protein.
OS Rana tigrina ranavirus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
OX NCBI_TaxID=160691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21874850; PubMed=11878922; DOI=10.1006/viro.2001.1245;
RA He J.G., Lu L., Deng M., He H.H., Weng S.P., Wang X.H., Zhou S.Y.,
RA Long Q.X., Wang X.Z., Chan S.M.;
RT "Sequence analysis of the complete genome of an iridovirus isolated
RT from the tiger frog";
RL Virology 292:185-197(2002).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
DR EMBL; AF389451; AAL77812.1; -; Genomic_DNA.
DR HSP; P45352; IRTS.
DR SMR; Q8QY23; 1-124.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0004799; F:thymidylate synthase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006231; P:dTMP biosynthesis; IEA.
DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.
DR InterPro; IPR000398; Thymidylat synth.
DR Pfam; PF00303; Thymidylat synth; 1.
DR PRINTS; PR00108; THYMDSNTHASE.
DR ProDom; PD001180; Thymidylat synth; 1.
SQ SEQUENCE 124 AA; 14002 MW; 7123A290B15E6D21 CRC64;

Query Match 85.7%; Score 48; DB 2; Length 124;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Matches	8	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	2	MALPCHA	9						

```

Db      141 MALPPCHA 148
|||||
RESULT 34
TYSB_BACAM
ID      TYSB_BACAM      STANDARD;      PRT;      264 AA.
AC      P54081;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-2000 (Rel. 39, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Thymidylate synthase B (EC 2.1.1.45) (TS B) (TSase B).
GN      Name=thyB; Synonyms=thyA;
OS      Bacillus anlyoliquefaciens.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1390;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC      STRAIN=ATCC 23844;
RA      Steinborn G., Richter K.;
RT      "Cloning of the Bacillus thymidylate synthase genes thyBA and thyBL.";
RL      Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC      biosynthesis (By similarity).
CC      -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC      dihydrofolate + dTMP.
CC      -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC      HSP; P00470; 1TYS.
CC      -!- SUBUNIT: Homodimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC
CC      EMBL; 250164; CA90532.1; ALT_INIT; Genomic_DNA.
DR      HSSP; P00470; 1TYS.
DR      HAMAP; MF_00008; -; 1.
DR      InterPro; IPR000398; Thymidylat synth.
DR      Pfam; PF00303; Thymidylat synth_1.
DR      PRINTS; PR001180; THYMDSNTHASE.
DR      ProDom; PS001180; Thymidylat synth; 1.
DR      PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW      Methyltransferase; THYMIDYLATE Family; Nucleotide biosynthesis;
KW      Transferase. 146 146 By similarity.
FT      ACT_SITE 146 146
SQ      SEQUENCE 264 AA; 30350 MW; 3092687D5653105B CRC64;
Query Match 85.7%; Score 48; DB 1; Length 264;
Best Local Similarity 88.9%; Pred. No. 3,2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      2 MALPPCHAL 10
|||||
Db      141 MALPPCHCL 149
|||||
RESULT 35
TYSB_BACSU
ID      TYSB_BACSU      STANDARD;      PRT;      264 AA.
AC      P11044;
DT      01-JUL-1989 (Rel. 11, Created)
DT      01-JUL-1989 (Rel. 11, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Thymidylate synthase B (EC 2.1.1.45) (TS B) (TSase B).
GN      Name=thyB; OrderedLocNames=BSU21820;
OS      Bacillus subtilis.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX      NCBI_TaxID=1423;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=168;
RX      MEDLINE=88284366; PubMed=2840350; DOI=10.1016/0378-1119(88)90476-3;
RA      Iwakura M., Kawata M., Tsuda K., Tanaka T.;
RT      "Nucleotide sequence of the thymidylate synthase B and dihydrofolate
RT      reductase genes contained in one Bacillus subtilis operon.";
RL      Gene 64:9-20(1988).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=168 / Marburg;
RX      MEDLINE=96349105; PubMed=8760912;
RA      Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
RA      Serror P.;
RT      "Sequence analysis of the Bacillus subtilis chromosome region between
RT      the serA and kds loci cloned in a yeast artificial chromosome.";
RL      Microbiology 142:2005-2016(1996).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=168, and ATCC 6633 / PCI 219;
RX      MEDLINE=93287974; PubMed=8510640;
RA      Montorsi M., Lorenzetti R.;
RT      "Heat-stable and heat-labile thymidylate synthases B of Bacillus
RT      subtilis: comparison of the nucleotide and amino acid sequences.";
RL      Mol. Gen. Genet. 239:1-5(1993).
RN      [4]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=168;
RX      MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA      Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA      Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA      Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA      Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA      Choi S.-K., Codani J.-J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA      Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA      Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA      Friz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA      Ghim S.-Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA      Guiseppi G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA      Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA      Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA      Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA      Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA      Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mael C.,
RA      Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA      Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA      Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA      Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA      Rey M., Reynolds S., Rieger M., Rivoita C., Rocha E., Roche B.,
RA      Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA      Scoffone F., Sekiguchi J., Sekowska A., Serror S.J., Serror P.,
RA      Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA      Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA      Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA      Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA      Weltzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA      Yoshikawa H., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RT      "The complete genome sequence of the Gram-positive bacterium Bacillus
RT      subtilis.";
RL      Nature 390:249-256(1997).
CC      -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC      biosynthesis.
CC      -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC      dihydrofolate + dTMP.
CC      -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC      Temperature dependence:
CC      Thermolabile. Inactive at 46 degrees Celsius;
CC      -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC      -!- SUBUNIT: Homodimer.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC      -!- MISCELLANEOUS: B.subtilis strain 168 possesses two thymidylate
CC      synthases, a major form thyA and a minor form thyB.
CC      -!- SIMILARITY: Belongs to the thymidylate synthase family.

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DR EMBL; X69661; CAM49350.1; -; Genomic_DNA.
 DR EMBL; L77246; AAA96634.1; -; Genomic_DNA.
 DR EMBL; M20012; AAA22852.1; -; Genomic_DNA.
 DR EMBL; Z99115; CAB14100.1; -; Genomic_DNA.
 DR PIR; J70250; SYB5TB.
 DR PIR; S35239; S35239.
 DR HSSP; P00470; IITYS.
 DR Subtilist; BG10794; thyB.
 DR HAMAP; MF_00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMDSNTASE.
 DR PRODOM; P000180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 DR Complete proteome; Methyltransferase; Multigene family;
 KW Nucleotide biosynthesis; Transferase.
 FT ACT_SITE 146 146
 FT VARIANT 7 37 F -> L (in strain ATCC 6633).
 FT VARIANT 37 39 N -> H (in strain ATCC 6633).
 FT VARIANT 39 39 R -> Q (in strain ATCC 6633).
 FT VARIANT 187 187 I -> M (in strain ATCC 6633).
 FT VARIANT 221 221 E -> T (in strain ATCC 6633).
 FT VARIANT 224 224 V -> L (in strain ATCC 6633).
 FT VARIANT 229 229 Q -> K (in strain ATCC 6633).
 FT VARIANT 229 229 V -> K (in strain ATCC 6633).
 FT VARIANT 235 236 KV -> EI (in strain ATCC 6633).
 SQ SEQUENCE 264 AA; 30538 MW; 1BPE1F1B8202E64 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
 |||||
 Db 141 MALPPCHCL 149

RESULT 36

IDSY AGRTS STANDARD; PRT; 264 AA.

AC Q8UDS3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA; OrderedLocuNames=Atu2047, AGR_C3709;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McClelland G.E., Palmieri A.,
 RA Raymond C., Rouse G., Saenjhimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 CC biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC -----

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 CC -----

DR EMBL; AE009155; AAL43039.1; -; Genomic_DNA.
 DR EMBL; AE008121; AAK87800.1; ALT_INIT; Genomic_DNA.
 DR PIR; A12827; A12827.
 DR HSSP; P00470; 1TRG.
 DR HAMAP; MF_00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMDSNTASE.
 DR PRODOM; P000180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 DR Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT_SITE 161 161 By similarity.
 SQ SEQUENCE 264 AA; 29875 MW; 9B44EDA6E73D3337 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
 |||||
 Db 141 MALPPCHCL 149

RESULT 37

IDSY BDEBA STANDARD; PRT; 264 AA.

AC Q6MID2;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thyA; OrderedLocuNames=Bd3230;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bdellovibrionaceae; Bdellovibrio.
 OX NCBI_TaxID=959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
 genomic perspective.";
 RL Science 303:689-692 (2004).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA


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CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX842655; CAE78047.1; -; Genomic_DNA.
CC HSP: P00470; LAXW. -; 1.
CC HAMAP: MF_00008; -; 1.
CC InterPro: IPR000398; Thymidylat_synth.
CC Pfam: PF00303; Thymidylat_synth; 1.
CC PRINTS: PR00108; THYMDSNTHASE.
CC PROSITE: PS001180; Thymidylat synth; 1.
CC PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferrase.
CC ACT SITE 146 146 By similarity.
CC SEQUENCE 264 AA; 30443 MW; 81229428565E102 CRC64;
CC -----
CC Query Match 85.7%; Score 48; DB 1; Length 264;
CC Best Local Similarity 100.0%; Pred. No. 3.2;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 2 MALPPCHA 9
CC Db 141 MALPPCHA 148
CC -----
CC RESULT 38
CC TSY BRAJA
CC ID TSY BRAJA STANDARD; PRT; 264 AA.
CC AC Q89G35.
CC DT 10-MAY-2005 (Rel. 47, Created)
CC DT 10-MAY-2005 (Rel. 47, Last sequence update)
CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
CC DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
CC GN Name=thvA; OrderedLocNames=bl16512;
CC OS Bradyrhizobium japonicum.
CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC OC Bradyrhizobiaceae; Bradyrhizobium.
CC OX NCBI_TaxID=375;
CC [1]
CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC RC STRAIN=USDA 110;
CC RX MEDLINE=22484998; PubMed=12597275;
CC RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
CC Sasamoto S., Watanabe A., Idesawa K., Irriguchi M., Kawashima K.,
CC Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
CC Tabata S.;
CC RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
CC Bradyrhizobium japonicum USDA110."
CC RL DNA Res. 9:189-197(2002).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC removed.
CC -----
CC EMBL: BA000040; BAC51777.1; -; Genomic_DNA.
CC HSP: P00470; ITYS. -; 1.
CC HAMAP: MF_00008; -; 1.
CC InterPro: IPR000398; Thymidylat_synth.
CC Pfam: PF00303; Thymidylat_synth; 1.
CC PRINTS: PR00108; THYMDSNTHASE.
CC PROSITE: PS001180; Thymidylat synth; 1.
CC PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferrase.
CC ACT SITE 146 146 By similarity.
CC SEQUENCE 264 AA; 29941 MW; 112056C0A989073F CRC64;
CC -----
CC Query Match 85.7%; Score 48; DB 1; Length 264;
CC Best Local Similarity 88.9%; Pred. No. 3.2;
CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 2 MALPPCHAL 10
CC Db 141 MALPPCHCL 149
CC -----
CC RESULT 39
CC TSY BRUME
CC ID TSY BRUME STANDARD; PRT; 264 AA.
CC AC P67042; Q8YI37;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 25-OCT-2004 (Rel. 45, Last sequence update)
CC DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
CC GN Name=thvA; OrderedLocNames=BMEI0608;
CC OS Brucella melitensis.
CC OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC OC Brucelliaceae; Brucella.
CC OX NCBI_TaxID=29459;
CC [1]
CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC RC STRAIN=16M / ATCC 23456 / Biotype 1;
CC RX MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
CC DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Mujer C., Los T.,
CC Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Resnik G.,
CC Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
CC Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
CC Haselkorn R., Kypides N.C., Overbeek R.;
CC RA "The genome sequence of the facultative intracellular pathogen
CC Brucella melitensis."
CC RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
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CC removed.
CC -----
CC EMBL: AE009503; AAL51789.1; -; Genomic_DNA.
CC FIR: AB3328; AB3328.
CC HSP: P00470; ITYS. -; 1.
CC HAMAP: MF_00008; -; 1.
CC InterPro: IPR000398; Thymidylat_synth.
CC Pfam: PF00303; Thymidylat synth; 1.
CC PRINTS: PR00108; THYMDSNTHASE.
CC PROSITE: PS001180; Thymidylat synth; 1.
CC PROSITE: PS00091; THYMIDYLATE SYNTHASE; 1.

```

KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 30330 MW; FECA558B5EDCAFA CRC64;

Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHCL 149

RESULT 40

QY TYSY BRUSU
 ID TYSY BRUSU STANDARD; PRT; 264 AA.
 AC P67043; Q8Y137;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thylA; OrderedLocuNames=BR1399;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Brucellaceae; Brucella.
 OX NCBI TaxID=29461;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
 RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
 RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
 RA Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 animal and plant pathogens and symbionts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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 removed.

EMBL; AE014436; AAN30312.1; -; Genomic_DNA.
 DR HSSP; P00470; 1TYS.
 DR TIGR; BR1399; -.
 DR HANAP; MF 00008; -; 1.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR Pfam; PF00303; Thymidylat_synth; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat_synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 30330 MW; FECA558B5EDCAFA CRC64;

Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHCL 149

RESULT 41

QY TYSY RHIL
 ID TYSY RHIL STANDARD; PRT; 264 AA.
 AC Q98KH9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thylA; OrderedLocuNames=ml11467;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Mesorhizobium.
 OX NCBI TaxID=381;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti";
 RL DNA Res. 7:331-338 (2000).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.

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EMBL; BA000012; BAB48835.1; -; Genomic_DNA.
 DR HSSP; P00470; 1TYS.
 DR HANAP; MF 00008; -; 1.
 DR InterPro; IPR000398; Thymidylat_synth.
 DR Pfam; PF00303; Thymidylat_synth; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat_synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 30096 MW; 8SD628F7A43300E0 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 DB 141 MALPPCHCL 149

RESULT 42

QY TYSY RHIME
 ID TYSY RHIME STANDARD; PRT; 264 AA.
 AC Q92NQ5;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thya; OrderedLocNames=R02127; ORFNames=SMC01444;
 OS Rhizobium meliloti (sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
 RX Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Anpe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
 RT "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC
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 CC removed.
 CC
 CC EMBL; AL591789; CAC46706.1; -; Genomic_DNA.
 DR HSP; P00470; ITRG.
 DR HAMAP; MF 00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMSNTSHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMYDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 FT Transferrase.
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 29987 MW; 056C72E2A9281123 CRC64;
 Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 DB 141 MALPPCHCL 149
 RESULT 43
 TYSY_RHOA
 ID TYSY_RHOA STANDARD; PRT; 264 AA.
 AC Q6N447;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thya; OrderedLocNames=RPA3493;
 OS Rhodospseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodospseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=CGA009 / ATCC BAA-98;

RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Petes C.,
 RA Harrison P.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 photosynthetic bacterium Rhodospseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC
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 CC removed.
 CC
 CC EMBL; BX572604; CAB28934.1; -; Genomic_DNA.
 DR HSP; P00470; IAXW.
 DR HAMAP; MF 00008; -; 1.
 DR InterPro; IPR000398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synt; 1.
 DR PRINTS; PR00108; THYMSNTSHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMYDYLATE SYNTHASE; 1.
 KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 FT Transferrase.
 FT ACT SITE 146 146 By similarity.
 SQ SEQUENCE 264 AA; 29662 MW; C42FEEDCBDCFCAD CRC64;
 Query Match 85.7%; Score 48; DB 1; Length 264;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 DB 141 MALPPCHCL 149
 RESULT 44
 Q57CA9_BRUAB
 ID Q57CA9_BRUAB PRELIMINARY; PRT; 264 AA.
 AC Q57CA9;
 DT 10-MAY-2005 (TREMELrel. 30, Created)
 DT 10-MAY-2005 (TREMELrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMELrel. 30, Last annotation update)
 DE Thya, thymidylate synthase.
 GN Name=thya; OrderedLocNames=Brub1_1394;
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=235;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=9-941 / Biovar 1;
 RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
 RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuercher R.L.,
 RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
 RT "Completion of the genome sequence of Brucella abortus and comparison
 to the highly similar genomes of Brucella melitensis and Brucella
 suis.";
 RL J. Bacteriol. 187:2715-2726(2005).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 DR EMBL; AB017223; AAX74725.1; -; Genomic_DNA.

```
DR GO: GO:0008168; F:methyltransferase activity; IEA.
DR GO: GO:0004799; F:thymidylate synthase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006231; F:dTMP biosynthesis; IEA.
DR GO: GO:0009165; P:nucleotide biosynthesis; IEA.
KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transferase.
SQ SEQUENCE 264 AA; 30330 MW; FECAD558B5EDCAFA CRC64;

Query Match      85.7%; Score 48; DB 2; Length 264;
Best Local Similarity 88.9%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 141 MALPPCHCL 149

RESULT 45
TYSY MYCLE
ID TYSY MYCLE STANDARD; PRT; 266 AA.
AC Q9CBW0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thylA; OrderedLocNames=ML1519;
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL583922; CAC30470.1; -; Genomic_DNA.
CC PIR; A87099; A87099.
CC HSP; P00470; 1TRG.
CC Leproma; ML1519; -.
CC HAMAP; MF 00008; -; 1.
CC InterPro; IPR000398; Thymidylat_synth.
CC Pfam; PF00303; Thymidylat_synth; 1.
CC PRINTS; PR00108; THYMDSNTHASE.
CC ProDom; PD001180; Thymidylat_synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferase.

QY 2 MALPPCHA 9
DB 144 MALPPCHA 151

RESULT 46
TYSY MYCPA
ID TYSY MYCPA STANDARD; PRT; 266 AA.
AC Q73VZ2;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
GN Name=thylA; OrderedLocNames=MAP2869c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017237; AAS05186.1; -; Genomic_DNA.
CC HSP; P00470; 1AXW.
CC HAMAP; MF 00008; -; 1.
CC InterPro; IPR000398; Thymidylat_synth.
CC Pfam; PF00303; Thymidylat_synth; 1.
CC PRINTS; PR00108; THYMDSNTHASE.
CC ProDom; PD001180; Thymidylat_synth; 1.
CC PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
CC Complete proteome; Methyltransferase; Nucleotide biosynthesis;
CC Transferase.
QY 2 MALPPCHA 9
DB 144 MALPPCHA 151

RESULT 47
Q4NHCB_9MICC
ID Q4NHCB_9MICC PRELIMINARY; PRT; 267 AA.
AC Q4NHCB;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
```

DT 13-SEP-2005 (TREMELrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMELrel. 31, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45).
 GN ORFNames=ArthDRAFT_2512;
 OS Arthrobacter sp. FB24.
 OC Bacteria; Actinobacteridae; Actinobacteriales;
 OC Micrococccineae; Micrococaceae; Arthrobacter.
 OX NCBI_TaxID=290399;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP STRAIN=PB24;
 RC US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lepidus A., Barry K., Glavina T.,
 RG Hammon N., Istrani S., Ptluck S., Richardson P.,
 RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2] NUCLEOTIDE SEQUENCE.
 RP STRAIN=PB24;
 RC US DOE Joint Genome Institute (JGI-PGF);
 RA Larimer F., Land M.,
 RG "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
 RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RL Submitter: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
 CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
 CC EMBL; AAHG01000004; BA096971.1; -; Genomic_DNA.
 DR InterPro; IPR00398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 DR Methyltransferase; Nucleotide biosynthesis; Transferase.
 KW SEQUENCE 267 AA; 30447 MW; 64DE7A588619AC66 CRC64;
 SQ
 Query Match 85.7%; Score 48; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 2 MALPPCHA 9
 DB 144 MALPPCHA 151
 RESULT 48
 ID TSY PROAC STANDARD; PRT; 269 AA.
 AC Q6A761;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thymidylate synthase (EC 2.1.1.45) (TS) (TSase).
 GN Name=thvA; OrderedLocNames=PPA1672;
 OS Propionibacterium acnes
 OC Bacteria; Actinobacteridae; Actinobacteriales;
 OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
 OX NCBI_TaxID=1747;
 RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=KPA171202 / DSM 16379;
 RC PubMed=15286373; DOI=10.1126/science.1100330;
 RA Bruggemann H., Henne A., Hostler F., Liesegang H., Wieser A.,
 RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
 RT "The complete genome sequence of Propionibacterium acnes, a commensal
 RT of human skin."
 RL Science 305:671-673 (2004).
 CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
 CC biosynthesis (By similarity).
 CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =

CC dihydrofolate + dTMP.
 CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
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 CC removed.
 CC EMBL; AE017283; AAT83404.1; -; Genomic_DNA.
 DR HAMAP; MF_00008; -; 1.
 DR InterPro; IPR00398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
 DR Complete proteome; Methyltransferase; Nucleotide biosynthesis;
 KW Transferase.
 FT ACT SITE 145 145 By similarity.
 SQ SEQUENCE 269 AA; 30838 MW; 80AFC40F5B687168 CRC64;
 Query Match 85.7%; Score 48; DB 1; Length 269;
 Best Local Similarity 88.9%; Pred. No. 3.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 DB 140 MALPPCHTL 148
 RESULT 49
 ID Q76YC2_9CAUD PRELIMINARY; PRT; 277 AA.
 AC Q76YC2;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE DTMP synthase.
 OS Bacteriophage Aehl.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OX NCBI_TaxID=227470;
 RN [1] NUCLEOTIDE SEQUENCE.
 RP Petrov V., Nolan J., Bertrand C., Letarov A.V., Krusch H.M.,
 RA Karam J.D.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 RN [2] NUCLEOTIDE SEQUENCE.
 RP Petrov V., Nolan J., Karam J.D.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY266303; AAQ17973.1; -; Genomic_DNA.
 DR HSP; P00470; IAXW.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:004799; F:thymidylate synthase activity; IEA.
 DR GO; GO:0016740; E:transferase activity; IEA.
 DR GO; GO:0006231; E:dTMP biosynthesis; IEA.
 DR InterPro; IPR00398; Thymidylat synth.
 DR Pfam; PF00303; Thymidylat synth; 1.
 DR PRINTS; PR00108; THYMDSNTHASE.
 DR ProDom; PD001180; Thymidylat synth; 1.
 SQ SEQUENCE 277 AA; 31538 MW; 28D5F3AB966EAF31 CRC64;
 Query Match 85.7%; Score 48; DB 2; Length 277;
 Best Local Similarity 88.9%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 MALPPCHAL 10
 DB 151 MALPPCHVL 159

```

RESULT 50
TVSY CAUCR
ID TVSY CAUCR STANDARD; PRT; 279 AA.
AC Q9AGH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thymidylate synthase (EC 2.1.1.45) (TS) (Tsase).
GN Name=thyA; OrderedLocusNames=CC2124;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- FUNCTION: Provides the sole de novo source of dTMP for DNA
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + dUMP =
CC dihydrofolate + dTMP.
CC -!- PATHWAY: Deoxyribonucleotide biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the thymidylate synthase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE005885; AAK24095.1; -; Genomic DNA.
DR PIR; C87512; C87512.
DR HSP; P00470; 1F4G.
DR TIGR; CC2124; -.
DR HAMAP; MF_00008; -.
DR InterPro; IPR00398; Thymidylat_synth.
DR Pfam; PF00303; Thymidylat_synt; 1.
DR PRINTS; PR00108; THYMDSNTHASE.
DR ProDom; PD001180; Thymidylat_synth; 1.
DR PROSITE; PS00091; THYMIDYLATE SYNTHASE; 1.
KW Complete proteome; Methyltransferase; Nucleotide biosynthesis;
KW Transferase.
FT ACT SITE 162 162 By similarity.
SQ SEQUENCE 279 AA; 31462 MW; 9EEE96984171B2D7 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 279;
Best Local Similarity 88.9%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
Db 157 MALPPCHCL 165

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Search completed: February 17, 2006, 02:44:03
 Job time : 267 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:36:16 ; Search time 186 Seconds
(without alignments)
23.623 Million cell updates/sec

Title: US-10-734-049B-188
Perfect score: 56
Sequence: 1 LMALPPCHAL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Listing first 1000 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	7	Adi15844 HLA-A2 re
2	56	100.0	216	4	Abg20769 Novel hum
3	56	100.0	230	7	Adc56779 Splice va
4	56	100.0	279	7	Adc56780 Splice va
5	56	100.0	284	5	Abp53743 Human thy
6	56	100.0	313	2	Aaw75754 Mutated t
7	56	100.0	313	2	Aaw75758 Mutated t
8	56	100.0	313	2	Aaw75755 Mutated t
9	56	100.0	313	2	Aaw75757 Mutated t
10	56	100.0	313	2	Aaw75766 Mutated t
11	56	100.0	313	2	Aaw75752 Mutated t
12	56	100.0	313	2	Aaw75763 Mutated t
13	56	100.0	313	2	Aaw75764 Mutated t
14	56	100.0	313	2	Aaw75755 Mutated t
15	56	100.0	313	2	Aaw75768 Mutated t
16	56	100.0	313	2	Aaw75762 Mutated t
17	56	100.0	313	2	Aaw75756 Mutated t
18	56	100.0	313	2	Aaw75759 Mutated t
19	56	100.0	313	2	Aaw75767 Mutated t
20	56	100.0	313	2	Aaw75760 Mutated t
21	56	100.0	313	2	Aaw75761 Mutated t
22	56	100.0	313	2	Aaw75753 Mutated t
23	56	100.0	313	5	Abp53744 Human thy
24	56	100.0	313	5	Aau87071 Human thy

25	56	100.0	313	7	ADC56778 Human thy
26	56	100.0	313	7	Ad222424 HLA-B46 T
27	56	100.0	313	7	Ade76649 Human thy
28	56	100.0	313	7	Ade76650 Human thy
29	56	100.0	313	7	Ade76628 Human thy
30	56	100.0	313	7	Ade76636 Human thy
31	56	100.0	313	7	Ade76643 Human thy
32	56	100.0	313	7	Ade76626 Human thy
33	56	100.0	313	7	Ade76647 Human thy
34	56	100.0	313	7	Ade76654 Human thy
35	56	100.0	313	7	Ade76655 Human thy
36	56	100.0	313	7	Ade76648 Human thy
37	56	100.0	313	7	Ade76651 Human thy
38	56	100.0	313	7	Ade76637 Human thy
39	56	100.0	313	7	Ade76631 Human thy
40	56	100.0	313	7	Ade76627 Human thy
41	56	100.0	313	7	Ade76630 Human thy
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44	56	100.0	313	7	Ade76641 Human thy
45	56	100.0	313	7	Ade76644 Human thy
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48	56	100.0	313	7	Ade76625 Human thy
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51	56	100.0	313	7	Ade76642 Human thy
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53	56	100.0	313	7	Ade76635 Human thy
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56	56	100.0	313	7	Adi15923 Human PP
57	56	100.0	313	8	Adn95029 Human thy
58	56	100.0	313	8	Ado19295 Human PRO
59	56	100.0	313	8	Adq18352 Human sof
60	56	100.0	313	8	Adq09248 Human TYM
61	56	100.0	313	9	Ady14832 PRO polyP
62	56	100.0	313	9	Aeb11762 Human thy
63	53	94.6	313	7	Ade76632 Human thy
64	52	92.9	257	6	Abp77914 N. gonorr
65	52	92.9	264	6	Abu38116 Protein e
66	52	92.9	264	6	Abu38239 Protein e
67	52	92.9	264	8	Adss1909 Thymidyla
68	52	92.9	264	8	Adss1911 Thymidyla
69	52	92.9	266	6	Abu37204 Protein e
70	52	92.9	289	7	Abu083049 Pseudomon
71	52	92.9	292	5	Abp66258 Bifidobac
72	51	91.1	337	2	Aaw23537 Kaposi sa
73	51	91.1	337	2	Aaw40100 Human her
74	51	91.1	337	2	Aaw52312 KSHV dihy
75	49	87.5	313	7	Ade76657 Human thy
76	49	87.5	314	5	Abb48389 Listeria
77	49	87.5	314	6	Abu33088 Protein e
78	48	85.7	263	6	Abu36845 Protein e
79	48	85.7	266	6	Abu34771 Protein e
80	48	85.7	266	6	Abu33878 Protein e
81	48	85.7	266	6	Abu35953 Protein e
82	48	85.7	270	4	Aau44958 Propionib
83	48	85.7	270	6	Abm41477 Propionib
84	48	85.7	285	4	Ag84982 Shrimp wh
85	48	85.7	313	7	Ade76633 Human thy
86	48	85.7	313	7	Ade76646 Human thy
87	48	85.7	314	6	Abu17459 Protein e
88	48	85.7	315	6	Adb07220 Alloioococ
89	48	85.7	316	5	Aam49496 Lactobaci
90	48	85.7	321	4	Abb59697 Drosophil
91	48	85.7	333	3	Aab53133 Macaca mu
92	48	85.7	350	7	Adb70074 C. neofo
93	48	85.7	375	8	Adx80283 plant ful
94	47	83.9	225	4	Aab0128 Coryneb
95	47	83.9	266	4	Aag90688 C glutami
96	47	83.9	266	4	Aae22710 Coryneb
97	47	83.9	279	6	Abu25747 Protein e

98	47	83.9	323	6	ABU39749	Abu39749 Protein e	171	40	71.4	440	4	ABG25231	Novel hum
99	47	83.9	323	6	ABU22997	Abu22997 Protein e	172	40	71.4	441	4	ABG25233	Novel hum
100	47	83.9	323	6	ABU41484	Abu41484 Protein e	173	39	69.6	57	4	AAU60176	Propionib
101	47	83.9	608	8	ADS75088	Ads75088 P. falcip	174	39	69.6	57	6	ABM56695	Propionib
102	47	83.9	612	7	AYL17271	Ayl17271 N. caninu	175	39	69.6	351	8	ADM94208	Wheat Dio
103	46	82.1	55	7	ADJ62279	Adj62279 Epitopic	176	39	69.6	1346	3	AAG39112	Arabidops
104	46	82.1	55	9	AEC10937	Aec10937 Enterococ	177	39	69.6	1390	3	AAG39111	Arabidops
105	46	82.1	315	6	ABU29298	Abu29298 Protein e	178	39	69.6	1403	3	AAG39110	Arabidops
106	46	82.1	315	7	ADJ62274	Adj62274 E. faecali	179	38	67.9	46	4	ABB40858	Peptide #
107	46	82.1	315	7	ADJ62276	Adj62276 E. faecali	180	38	67.9	46	4	AAAM34626	Peptide #
108	46	82.1	315	9	AEC10932	Aec10932 Enterococ	181	38	67.9	46	4	AAAM74513	Human bra
109	46	82.1	315	9	AEC10934	Aec10934 Enterococ	182	38	67.9	46	4	AAAM61717	Human bra
110	46	82.1	318	6	ABU42652	Abu42652 Protein e	183	38	67.9	46	4	ABG56304	Human liv
111	46	82.1	318	6	ABU42411	Abu42411 Protein e	184	38	67.9	55	4	AAAM33030	Peptide #
112	46	82.1	318	6	ABU42887	Abu42887 Protein e	185	38	67.9	55	4	AAAM72800	Human bon
113	46	82.1	318	6	ABU43921	Abu43921 Protein e	186	38	67.9	55	4	AAAM60182	Human bra
114	46	82.1	318	9	ADM94714	Adm94714 Prolifera	187	38	67.9	55	4	ABG54501	Human liv
115	46	82.1	322	5	ABP38349	Abp38349 Staphyloc	188	38	67.9	55	5	ABG42625	Human pep
116	46	82.1	322	5	ABM73020	Abm73020 Staphyloc	189	38	67.9	88	3	AAG13004	Arabidops
117	46	82.1	324	7	ADH86518	Adh86518 E. faecali	190	38	67.9	99	3	AAG13003	Arabidops
118	46	82.1	325	7	ADH86461	Adh86461 Enterococ	191	38	67.9	110	3	AAG07125	Arabidops
119	45	80.4	142	7	ADH73100	Adh73100 Human cel	192	38	67.9	119	6	ADA55319	Human pro
120	44	78.6	51	8	ADU16623	Adu16623 M. tuberc	193	38	67.9	121	3	AAAG07124	Arabidops
121	44	78.6	75	5	ABP05623	Abp05623 Human ORF	194	38	67.9	127	5	ABP64011	Human ORF
122	44	78.6	93	5	ABP34334	Abp34334 Human syn	195	38	67.9	132	3	AAAG07123	Arabidops
123	44	78.6	97	8	ADU06836	Adu06836 Cell adhe	196	38	67.9	142	3	AAAB18666	Human r
124	44	78.6	116	2	AAU04823	Aau04823 Mycobacte	197	38	67.9	147	4	ABU52774	Human bra
125	44	78.6	119	2	AAU04823	Aau04823 Mycobacte	198	38	67.9	147	4	ABG27392	Novel hum
126	44	78.6	136	5	ABP63828	Abp63828 Human ORF	199	38	67.9	232	5	ABBA47727	Listeria
127	44	78.6	184	2	AAW06581	Aaw06581 Mouse uro	200	38	67.9	242	7	ADD18574	Human dis
128	44	78.6	184	2	AAU21547	Aau21547 Mouse uro	201	38	67.9	242	7	ADD18574	Human dis
129	44	78.6	184	3	AAU51073	Aau51073 Murine UP	202	38	67.9	242	8	ADO24543	Human PRO
130	44	78.6	184	4	AAU79102	Aau79102 Amino aci	203	38	67.9	395	8	ADS14973	Pseudomon
131	44	78.6	184	4	AAU79166	Aau79166 Human pro	204	38	67.9	1101	8	ADJ45097	Rice isop
132	44	78.6	184	5	AAU74525	Aau74525 Human uro	205	37	66.1	60	5	AAU83521	Novel hum
133	44	78.6	184	6	ABR48166	AbR48166 Human bla	206	37	66.1	76	4	AAU19213	Human ORF
134	44	78.6	184	7	ADN38855	Adn38855 Cancer/an	207	37	66.1	84	5	ABP33952	Human G P
135	44	78.6	196	4	AAAM80150	Aam80150 Human pro	208	37	66.1	167	4	AAU63465	Propionib
136	44	78.6	280	6	ABU35270	Abu35270 Protein e	209	37	66.1	167	6	ABM59984	Propionib
137	44	78.6	280	6	ABU17232	Abu17232 Protein e	210	37	66.1	167	6	ABM65523	Propionib
138	44	78.6	282	8	ADL04890	Adl04890 M. catarr	211	37	66.1	279	8	ADT58342	Plant pol
139	44	78.6	286	6	ADA36773	Ada36773 Acinetoba	212	37	66.1	346	4	ABB68782	Drosophil
140	44	78.6	315	5	ABP73399	Abp73399 Candida a	213	37	66.1	388	8	ADY09852	Plant ful
141	44	78.6	328	6	ABU36316	Abu36316 Protein e	214	37	66.1	396	4	ABG28659	Novel hum
142	44	78.6	340	5	ADH32879	Adh32879 Yeast smo	215	37	66.1	984	7	ABM88980	Rice abio
143	44	78.6	344	6	ABJ25585	Abj25585 Aspergill	216	37	66.1	9913	8	ADT40977	HSARS vir
144	44	78.6	344	6	ABJ26185	Abj26185 Aspergill	217	37	66.1	9913	8	ADT38507	HSARS vir
145	43	75.8	52	8	ADS51915	Ads51915 Thymidyla	218	37	66.1	9913	9	ABE00352	SARS coro
146	43	75.8	161	9	ABM95094	Abm95094 M. xanthu	219	36	64.3	7	8	ADT40999	HSARS vir
147	43	76.8	264	9	ABE40796	AbE40796 L. pneumo	220	36	64.3	7	8	ADS80414	SARS viru
148	43	76.8	265	9	ABE37482	AbE37482 L. pneumo	221	36	64.3	7	8	ADT38529	HSARS vir
149	42	75.0	264	6	ABU20990	Abu20990 Protein e	222	36	64.3	7	8	ADT38529	HSARS vir
150	42	75.0	277	9	AEA51131	Aea51131 Pseudomon	223	36	64.3	48	4	ABE64316	Drosophil
151	41	73.2	287	6	ABU35594	Abu35594 Protein e	224	36	64.3	120	4	AAAG92569	C Glutami
152	40.5	72.3	218	2	AAW44089	Aaw44089 Human sec	225	36	64.3	190	3	AAAB25689	Human sec
153	40.5	72.3	218	2	AAW27653	Aaw27653 Secreted	226	36	64.3	237	4	ABE70652	Drosophil
154	40.5	72.3	218	3	AAAB10234	Aab10234 Human fet	227	36	64.3	246	9	ABM95836	M. xanthu
155	40.5	72.3	226	4	ADM19928	Adm19928 Protein e	228	36	64.3	289	8	ADO08181	Human ful
156	40.5	72.3	398	7	ADC131835	Adc131835 Human nov	229	36	64.3	318	8	ADV26402	Human Fz1
157	40.5	72.3	542	5	AAU74356	Aau74356 Human cyt	230	36	64.3	351	8	ADY13196	Plant ful
158	40.5	72.3	645	7	ADCL10136	Adcl10136 Human NOV	231	36	64.3	455	8	ADP29417	Human sec
159	40	71.4	105	5	ABP00422	Abp00422 Human ORF	232	36	64.3	463	9	ADP29417	Human sec
160	40	71.4	118	7	ABO67777	AbO67777 Klebsiell	233	36	64.3	544	7	ADG74255	Rat frizz
161	40	71.4	264	4	AGS98326	AgS98326 Escherich	234	36	64.3	596	2	AAW48785	Thyroid p
162	40	71.4	264	6	ABU32203	Abu32203 Protein e	235	36	64.3	626	7	ADG74260	Mouse fri
163	40	71.4	264	6	ABU14834	Abu14834 Protein e	236	36	64.3	635	6	ABG74260	Mouse fri
164	40	71.4	264	6	ABU50438	Abu50438 Protein e	237	36	64.3	635	6	ABU50596	Protein e
165	40	71.4	264	6	ABU45233	Abu45233 Protein e	238	36	64.3	642	8	ABW67514	Mouse GPC
166	40	71.4	264	6	ABU27963	Abu27963 Protein e	239	36	64.3	642	8	ABW67514	Mouse GPC
167	40	71.4	264	6	ABU48277	Abu48277 Protein e	240	36	64.3	647	9	AEA55061	Mouse fri
168	40	71.4	265	6	ABM67522	Abm67522 Photorhab	241	36	64.3	647	9	AAAB12117	Hydrophob
169	40	71.4	266	7	ABO63538	AbO63538 Klebsiell	242	36	64.3	647	6	ABU55896	Human pro
170	40	71.4	417	4	ABG25232	Abg25232 Novel hum	243	36	64.3	647	6	AAE34050	FZD1 prot

244	36	64.3	647	7	ADG74259	Human	frl	317	35	62.5	323	6	ABU21303	Abu21303 Protein e
245	36	64.3	647	7	ADP65222	Human	frl	318	35	62.5	328	6	ABU22494	Abu22494 Protein e
246	36	64.3	647	8	ADO22252	Human	F2D	319	35	62.5	332	6	ABU24530	Abu24530 Human ORF
247	36	64.3	648	8	ADO29693	Human	GPC	320	35	62.5	339	6	ABU20292	Abu20292 Protein e
248	36	64.3	648	9	AE288125	Human	Fri	321	35	62.5	344	7	AD814373	Ad814373 Human int
249	36	64.3	666	9	ABM88902	Rice	abio	322	35	62.5	352	7	ADC87349	Adc87349 Human GPC
250	36	64.3	681	2	AAW48786	Thyroid	p	323	35	62.5	353	3	AA82741	Aa82741 DNA repli
251	36	64.3	683	8	ADY10945	Plant	ful	324	35	62.5	353	4	AA894230	Aa894230 Human pro
252	36	64.3	689	2	AAW48787	Thyroid	p	325	35	62.5	353	5	AA668351	Aa668351 Human mit
253	36	64.3	784	2	AAW48783	Thyroid	p	326	35	62.5	353	6	ADA03123	Ada03123 Nucleotid
254	36	64.3	785	8	ABM83658	Human	dia	327	35	62.5	353	8	ADU60347	Adu60347 Housekeep
255	36	64.3	842	8	ABM83657	Human	dia	328	35	62.5	353	8	ADU07837	Adu07837 Cyclin-de
256	36	64.3	848	2	AAW07733	Human	thy	329	35	62.5	377	9	ADN24167	Adn24167 Bacterial
257	36	64.3	852	2	AAW48782	Thyroid	p	330	35	62.5	397	4	ABQ76949	Abq76949 Pseudomon
258	36	64.3	888	7	AD47732	Human	NOV	331	35	62.5	447	4	ABG14802	Abg14802 Novel hum
259	36	64.3	888	8	ADJ79002	Human	NOV	332	35	62.5	557	4	AB862937	Ab862937 Drosophil
260	36	64.3	924	2	AA835445	Human	TPO	333	35	62.5	592	4	ABG04091	Abg04091 Novel hum
261	36	64.3	933	2	AA844615	Human	thy	334	35	62.5	611	4	ABG19321	Abg19321 Novel hum
262	36	64.3	933	2	AA832875	Human	TPO	335	35	62.5	728	4	ABG03634	Abg03634 Novel hum
263	36	64.3	933	2	AA875689	Human	thr	336	35	62.5	839	5	AAE23384	Aae23384 Human int
264	36	64.3	933	7	ADJ68762	Human	hea	337	35	62.5	878	8	ADS25408	Ads25408 Bacterial
265	36	64.3	933	8	ADQ14321	Human	thy	338	35	62.5	1104	8	ADS26174	Ads26174 Bacterial
266	36	64.3	933	8	ADR41768	Human	thy	339	35	62.5	1104	8	ADS22427	Ads22427 Bacterial
267	36	64.3	933	8	ADS14361	Human	thy	340	35	62.5	1104	8	ADS25693	Ads25693 Bacterial
268	36	64.3	933	9	AB877781	Human	thy	341	35	62.5	1121	6	ADA26484	Ada26484 Alpha-iso
269	36	64.3	948	2	AAW48781	Thyroid	p	342	35	62.5	1465	4	ABM88297	Abm88297 Rice abio
270	36	64.3	956	9	ABM91196	M. xanthu		343	35	62.5	1624	7	ABM60544	Abm60544 Drosophil
271	36	64.3	992	2	AA873917	Rubella	v	344	35	62.5	1624	8	ADL91596	Adl91596 Drosophil
272	36	64.3	1222	4	AB858342	Drosophil		345	35	62.5	1662	7	AD808526	Ad808526 Novel pro
273	36	64.3	4601	4	AB859371	Drosophil		346	35	62.5	2042	7	ADM25528	Adm25528 Hyperther
274	35	62.5	14	9	AEA35162	LPS bindi		347	35	62.5	4660	8	ADM21713	Adm21713 Rat LRP b
275	35	62.5	14	9	AEA35153	LPS bindi		348	34	60.7	16	5	AB888471	Ab888471 C aulicus
276	35	62.5	15	5	AAO18165	Human	ema	349	34	60.7	65	5	AB888382	Ab888382 C aulicus
277	35	62.5	24	4	ADL92085	Brain	der	350	34	60.7	68	5	ABP06409	Abp06409 Human ORF
278	35	62.5	54	4	AAU56776	Propionib		351	34	60.7	70	4	AA821267	AA821267 Peptide #
279	35	62.5	54	6	ABM53295	Propionib		352	34	60.7	70	4	AB843600	AB843600 Peptide #
280	35	62.5	59	5	AAW49806	Human	HPD	353	34	60.7	70	4	AAW37494	AAW37494 Peptide #
281	35	62.5	67	6	AAU48165	Propionib		354	34	60.7	70	4	AB826554	AB826554 Protein #
282	35	62.5	67	6	ABM44684	Propionib		355	34	60.7	70	4	AAW77344	AAW77344 Human bon
283	35	62.5	69	5	ABP64191	Human	ORF	356	34	60.7	70	4	AAW64539	AAW64539 Human bra
284	35	62.5	91	4	ABG02864	Novel	hum	357	34	60.7	70	4	ABG58976	Abg58976 Human liv
285	35	62.5	107	4	AAU32636	Novel	hum	358	34	60.7	70	5	ABG46359	Abg46359 Human pep
286	35	62.5	114	5	AAO18164	Human	ema	359	34	60.7	74	4	AA880322	AA880322 Human pro
287	35	62.5	116	4	AAU52367	Propionib		360	34	60.7	85	4	AA866845	AA866845 Human rib
288	35	62.5	116	6	ABM48886	Propionib		361	34	60.7	101	1	AA860357	AA860357 Sequence
289	35	62.5	129	4	AB847098	Protein	e	362	34	60.7	101	1	AA860357	AA860357 Interfero
290	35	62.5	134	8	ADJ49203	Oil-assoc		363	34	60.7	105	4	AAO04294	AAO04294 Human pol
291	35	62.5	138	4	AAU50183	Propionib		364	34	60.7	111	7	ADM64204	Adm64204 Human pro
292	35	62.5	138	6	ABM46702	Propionib		365	34	60.7	111	7	ADM04429	Adm04429 Human pro
293	35	62.5	151	5	AA868341	Human	gua	366	34	60.7	112	5	AB890100	AB890100 Human pol
294	35	62.5	157	6	ADA54939	Human	pro	367	34	60.7	112	9	AEA23369	Aea23369 Tumor ant
295	35	62.5	157	8	ADW87343	Human	pro	368	34	60.7	133	5	AAW47984	AAW47984 Human cyt
296	35	62.5	158	8	ADW93673	Plant	ful	369	34	60.7	149	4	AAU19286	AAU19286 Human G p
297	35	62.5	159	4	AAW25961	Human	pro	370	34	60.7	150	6	ADW54999	ADW54999 Human pro
298	35	62.5	159	8	ADW87789	Human	EST	371	34	60.7	152	7	ADC42860	Adc42860 REMAP pro
299	35	62.5	195	6	ADA55707	Human	pro	372	34	60.7	160	4	AA893921	AA893921 Human gen
300	35	62.5	196	6	ABR48157	Human	bla	373	34	60.7	167	6	AAE37059	AAE37059 Human gen
301	35	62.5	196	6	ABR48158	Human	bla	374	34	60.7	170	8	ADW78019	Adw78019 Plant ful
302	35	62.5	196	7	ADW38840	Cancer/an		375	34	60.7	175	8	ADW78975	Adw78975 Plant ful
303	35	62.5	196	7	ADW99570	Novel	hum	376	34	60.7	183	6	ABP56884	ABP56884 Xenopus C
304	35	62.5	196	9	ADY19522	PRO	polyp	377	34	60.7	184	7	ADW56862	ADW56862 Human GPC
305	35	62.5	196	9	ADY15592	PRO	polyp	378	34	60.7	186	8	ADP09671	Adp09671 Sheep cor
306	35	62.5	196	9	ADY72866	Human	cor	379	34	60.7	190	1	AA840294	AA840294 Human pro
307	35	62.5	202	9	ADW07036	Cyclin-de		380	34	60.7	195	8	ADQ66744	Adq66744 Novel hum
308	35	62.5	215	7	ADW26545	Hyperther		381	34	60.7	202	4	AAW25439	AAW25439 Human pro
309	35	62.5	229	4	AAW39526	Human	pol	382	34	60.7	222	4	ABG27005	Abg27005 Novel hum
310	35	62.5	252	7	ADW58746	Human	pol	383	34	60.7	242	6	AAE36182	Aae36182 Human CGD
311	35	62.5	264	4	ABG19781	Novel	hum	384	34	60.7	251	8	ADO08187	Ado08187 Human Fri
312	35	62.5	281	9	ABM97038	M. xanthu		385	34	60.7	251	9	ADW26408	Adw26408 Human Fri
313	35	62.5	294	7	ADC51446	Interfero		386	34	60.7	266	7	ADW08394	Adw08394 Novel pro
314	35	62.5	298	4	AAW41312	Human	pol	387	34	60.7	287	5	AAE17485	Aae17485 Human leu
315	35	62.5	306	7	ABO84010	Pseudomon		388	34	60.7	287	5	ABG69637	Abg69637 Human sec
316	35	62.5	308	8	ADW69062	Plant	ful	389	34	60.7	287	5	AAU83129	Aau83129 Novel sec

330	34	60.7	295	7	ADB85214	AdB85214	Rat chimia	463	33	58.9	23	2	AAW66468	AAW66468	Cationic
331	34	60.7	311	5	AAE23982	Aae23982	Human LP2	464	33	58.9	23	3	AAy91767	AAy91767	Cationic
332	34	60.7	341	8	ADT57699	Adt57699	Plant pol	465	33	58.9	23	6	ABU59645	ABU59645	Cationic
333	34	60.7	343	5	ADJ33317	Adj33317	Human pot	466	33	58.9	23	9	ADY67516	ADY67516	Tumor cel
334	34	60.7	365	6	AAE37076	Aae37076	Human gen	467	33	58.9	54	4	AAU39503	AAU39503	Propionib
335	34	60.7	392	7	ADB74461	AdB74461	Mycobacte	468	33	58.9	54	6	ABM36022	ABM36022	Propionib
336	34	60.7	411	6	ADA54098	Ada54098	Human pro	469	33	58.9	60	7	ADH86209	ADH86209	Enterococ
337	34	60.7	411	7	ADJ70680	Adj70680	Human hea	470	33	58.9	61	7	ADF04788	ADF04788	Bacterial
338	34	60.7	425	8	ADM87642	Adm87642	Human est	471	33	58.9	65	6	ADA33968	Ada33968	Acinetoba
339	34	60.7	455	7	ABM89085	Abm89085	Rice abio	472	33	58.9	67	6	ADA57293	Ada57293	Human sec
400	34	60.7	466	6	ABR58660	AbR58660	Human can	473	33	58.9	67	6	ADA41173	Ada41173	Human sec
401	34	60.7	467	5	AAO16105	Aao16105	Human act	474	33	58.9	67	7	ADC74375	AdC74375	Human sec
402	34	60.7	468	7	ADE59897	Ade59897	Human pro	475	33	58.9	69	7	ADF04113	AdF04113	Bacterial
403	34	60.7	499	8	ADM87184	Adm87184	Human pro	476	33	58.9	75	5	ADH32461	AdH32461	Yeast smO
404	34	60.7	512	7	ADG74270	Adg74270	Mouse fri	477	33	58.9	78	4	AAU91027	AAU91027	Human imm
405	34	60.7	515	7	ABM85921	Abm85921	Rice abio	478	33	58.9	79	4	AAU65381	AAU65381	Propionib
406	34	60.7	529	5	ABB07502	Abb07502	Human GTP	479	33	58.9	79	6	ABM61900	ABM61900	Propionib
407	34	60.7	545	5	AGS59376	AgS59376	Human DTP	480	33	58.9	82	3	ABM54363	ABM54363	Human pan
408	34	60.7	547	4	AAG67550	Aag67550	Amino aci	481	33	58.9	82	3	ABG54363	ABG54363	Human col
409	34	60.7	547	8	ADR09923	AdR09923	Human pro	482	33	58.9	85	8	ADY11334	AdY11334	Plant ful
410	34	60.7	572	2	AAW31273	Aaw31273	Mouse fri	483	33	58.9	97	5	ABP07985	ABP07985	Human ORF
411	34	60.7	572	8	ADO29338	Ado29338	Mouse GPC	484	33	58.9	99	6	ABR56776	ABR56776	Human sec
412	34	60.7	572	9	ADZ13020	Adz13020	Murine ca	485	33	58.9	101	4	AAU58381	AAU58381	Propionib
413	34	60.7	574	6	ABU55902	Abu55902	Human pro	486	33	58.9	101	6	ABM54900	ABM54900	Propionib
414	34	60.7	574	6	AAE34056	Aae34056	F2D7 prot	487	33	58.9	101	8	ADR09672	AdR09672	Human pro
415	34	60.7	574	7	ADG74269	Adg74269	Human fri	488	33	58.9	105	3	AAAB42868	AAaB42868	Human dig
416	34	60.7	574	8	ADN03982	Adn03982	Antipsori	489	33	58.9	106	4	AAU92229	AAU92229	Human ner
417	34	60.7	574	8	ADO29337	Ado29337	Human GPC	490	33	58.9	116	4	ABB16212	ABb16212	Human imm
418	34	60.7	574	8	ADO22264	Ado22264	Human F2D	491	33	58.9	122	4	AAU86426	AAU86426	Human imm
419	34	60.7	574	8	AQO18261	Aqo18261	Human sof	492	33	58.9	123	8	ADW80359	ADw80359	Human pro
420	34	60.7	574	8	ADU92964	AdU92964	Frizzled	493	33	58.9	128	4	ABG02051	ABg02051	Novel hum
421	34	60.7	574	8	ADU06307	Adu06307	Novel bro	494	33	58.9	128	8	ADX76105	ADx76105	Plant ful
422	34	60.7	574	9	ADZ13023	Adz13023	Human can	495	33	58.9	131	8	ABO57453	ABO57453	Human gen
423	34	60.7	574	9	ABE28131	Aeb28131	Human Fri	496	33	58.9	150	4	AAU93458	AAu93458	Human pro
424	34	60.7	595	4	ABB60297	Abb60297	Drosophil	497	33	58.9	150	8	ADL31083	ADL31083	Human pol
425	34	60.7	610	4	AGB06352	Agb06352	Novel hum	498	33	58.9	153	2	AAU13016	AAu13016	Deacetyl
426	34	60.7	629	7	ADH54846	Adh54846	Human ins	499	33	58.9	157	4	AAE03257	AAe03257	Human gen
427	34	60.7	666	4	ABB11769	Abb11769	Human du3	500	33	58.9	160	9	ADY22154	AdY22154	Rat immun
428	34	60.7	666	4	AAU79751	Aau79751	Human pro	501	33	58.9	164	4	AAAB93502	AAAB93502	Human pro
429	34	60.7	693	7	ABM85550	Abm85550	Mouse pro	502	33	58.9	165	7	ADM25800	Adm25800	Hyperther
430	34	60.7	764	5	ABO05596	AbO05596	Human tes	503	33	58.9	167	4	AAU63978	AAU63978	Propionib
431	34	60.7	769	8	ABO59732	AbO59732	Human gen	504	33	58.9	167	4	ABG02049	ABg02049	Novel hum
432	34	60.7	814	8	ADR22503	Adr22503	Human tra	505	33	58.9	167	6	ABM60497	ABm60497	Propionib
433	34	60.7	829	8	ADU99456	AdU99456	Human kin	506	33	58.9	169	5	ABB89348	ABb89348	Human pol
434	34	60.7	830	8	ADU99459	AdU99459	Murine ki	507	33	58.9	179	4	AAU21047	AAu21047	Human nov
435	34	60.7	842	8	AAU93306	Aau93306	Human pol	508	33	58.9	180	4	AAAB03223	AAAB03223	Human gen
436	34	60.7	842	8	ADL32020	Adl32020	Human pro	509	33	58.9	180	5	ABG64391	ABg64391	Human alb
437	34	60.7	945	4	AAU03538	Aau03538	Human pro	510	33	58.9	180	5	ABP64543	ABP64543	Human ORF
438	34	60.7	945	5	AAE19157	Aae19157	Human kin	511	33	58.9	180	8	ADL77658	ADl77658	Albumin f
439	34	60.7	965	9	ADV97905	Adv97905	Murine pr	512	33	58.9	185	4	AAE03256	AAe03256	Human gen
440	34	60.7	971	7	ADI63116	Adi63116	Human apo	513	33	58.9	190	4	AAE03255	AAE03255	Human gen
441	34	60.7	976	5	ABP35659	Abp35659	Fungal ZB	514	33	58.9	197	6	ABR58512	ABr58512	Human sec
442	34	60.7	982	8	ADJ96663	Adj96663	Human tyr	515	33	58.9	202	6	ABJ19779	ABj19779	Human MP2
443	34	60.7	1000	6	ABU62810	Abu62810	Human Gli	516	33	58.9	202	6	ABU89815	ABu89815	Deatch as
444	34	60.7	1127	4	ABG22813	Abg22813	Novel hum	517	33	58.9	202	8	ADO09417	AdO09417	Novel hum
445	34	60.7	1147	8	ADH22510	Adh22510	Human tra	518	33	58.9	202	8	ABO59922	ABO59922	Human gen
446	34	60.7	1163	7	ADK18350	Adk18350	Human NOV	519	33	58.9	204	3	AAAB56614	AAAB56614	Human pro
447	34	60.7	1163	7	ADM29274	Adm29274	Human nov	520	33	58.9	211	7	ABO69660	ABO69660	Pseudomon
448	34	60.7	1180	5	AAU91183	Aau91183	Human HEA	521	33	58.9	225	8	ABO59291	ABO59291	Human gen
449	34	60.7	1180	7	ABR62331	AbR62331	Human cat	522	33	58.9	253	6	ABU38204	ABu38204	Protein e
450	34	60.7	1180	7	ADK18348	Adk18348	Human NOV	523	33	58.9	256	8	ADS28721	ADs28721	Bacterial
451	34	60.7	1180	7	ADM29272	Adm29272	Human nov	524	33	58.9	264	7	ABO69341	ABO69341	Pseudomon
452	34	60.7	1180	8	ADI79949	Adi79949	Protein o	525	33	58.9	269	8	ADR51331	ADR51331	Anti-biof
453	34	60.7	1239	6	ABU48705	Abu48705	Human Gli	526	33	58.9	271	4	AAAB98360	AAAB98360	Cat SCF p
454	34	60.7	1596	5	AAO17114	Aao17114	Human tra	527	33	58.9	271	4	AAU02486	AAu02486	Cat SCF (
455	34	60.7	1596	8	ADO17743	Ado17743	Human sof	528	33	58.9	271	4	AAU02772	AAu02772	Cat SCF (
456	34	60.7	1597	9	AEA27510	Aea27510	Human zin	529	33	58.9	271	4	AAU05259	AAu05259	Cat stem
457	34	60.7	1597	9	AEA30113	Aea30113	Globulat	530	33	58.9	271	7	ADP99322	ADp99322	Cat stem
458	34	60.7	1774	8	ADR10354	Adr10354	Human pro	531	33	58.9	271	8	ADU50652	ADu50652	Cat stem
459	34	60.7	1862	8	ADH39685	Adh39685	Streptom	532	33	58.9	271	8	ADU50652	ADu50652	Cat stem
460	34	60.7	1995	8	ADL26784	Adl26784	Human Shr	533	33	58.9	271	9	ADW93097	ADw93097	Cat stem
461	34	60.7	3913	6	ABM67350	Abm67350	Photorhab	534	33	58.9	271	9	ADZ47549	ADz47549	Cat stem
462	33.5	58.8	741	8	ADS42307	AdS42307	Bacterial	535	33	58.9	271	9	ADZ47549	ADz47549	Cat stem

536	33	58.9	273	7	ABO68701	Abc68701 Pseudomon	609	33	58.9	778	5	ABP70144	Abp70144 Human NOV
537	33	58.9	274	2	AAW00979	Aaw00979 Feline st	610	33	58.9	781	4	ABG14738	Abg14738 Novel hum
538	33	58.9	274	4	AA96945	Aab96945 Cat stem	611	33	58.9	793	8	ABO59284	Abc59284 Human gen
539	33	58.9	274	9	AD247607	Adz47607 Cat stem	612	33	58.9	814	4	ABR12360	Abb12360 Human bon
540	33	58.9	287	8	ADX0889	Adx0889 Plant ful	613	33	58.9	814	5	ABP69266	Abp69266 Human pol
541	33	58.9	296	6	ABP98320	Abp98320 Amino aci	614	33	58.9	835	4	ABP94372	Abp94372 Human pro
542	33	58.9	300	8	ABU92057	Abu92057 Human pro	615	33	58.9	842	7	ADD18996	Adi18996 Human dis
543	33	58.9	303	8	ADY11741	Ady11741 Plant ful	616	33	58.9	889	9	ADW42864	Adw42864 Human cor
544	33	58.9	312	8	ADQ65470	Adq65470 Novel hum	617	33	58.9	900	9	ADW42857	Adw42857 Human cor
545	33	58.9	313	8	ADX65974	Adx65974 Plant ful	618	33	58.9	909	5	AAU72904	Aau72904 Human met
546	33	58.9	320	7	ADB74340	Adb74340 Mycobacte	619	33	58.9	910	3	ABR25104	Abp25104 Pinus rad
547	33	58.9	324	8	ADP25089	Adp25089 PRO polyP	620	33	58.9	927	7	ABM87868	Abm87868 Rice abio
548	33	58.9	329	8	ADOS1716	Ados1716 Streptomy	621	33	58.9	928	8	ADN20558	Adn20558 Bacterial
549	33	58.9	334	5	ABP41389	Abp41389 Human ova	622	33	58.9	955	7	ABO75508	Abc75508 Pseudomon
550	33	58.9	343	6	ADA34527	Ada34527 Acinetoba	623	33	58.9	991	9	ADW42876	Adw42876 Protein o
551	33	58.9	347	4	ABR68392	Abb68392 Drosophil	624	33	58.9	1006	7	ADW47700	Adw47700 Human NOV
552	33	58.9	349	5	ABR43860	Abp43860 MGC: 1127	625	33	58.9	1006	8	ADJ78970	Adj78970 Human NOV
553	33	58.9	359	4	AAE03206	Aae03206 Human gen	626	33	58.9	1030	4	ABG23699	Abg23699 Novel hum
554	33	58.9	359	5	ABG64393	Abg64393 Human alb	627	33	58.9	1039	9	ADW42872	Adw42872 Human cor
555	33	58.9	359	8	ADL77660	Adl77660 Albumin f	628	33	58.9	1042	3	AAU44426	Aau44426 Human ser
556	33	58.9	368	2	AAV41496	Aav41496 Fragment	629	33	58.9	1042	4	AAE06939	Aae06939 Human cor
557	33	58.9	379	4	ABR75212	Abp75212 Drosophil	630	33	58.9	1042	7	ADI10398	Adi10398 Human cel
558	33	58.9	379	5	AAE30514	Aae30514 Fruit fly	631	33	58.9	1042	8	ADJ46922	Adj46922 Human tra
559	33	58.9	403	7	ADM26461	Adm26461 Hyperther	632	33	58.9	1042	8	ADR29373	Adr29373 Human cor
560	33	58.9	413	4	AAU29772	Aau29772 Novel hum	633	33	58.9	1042	8	ADW42844	Adw42844 Human cor
561	33	58.9	429	8	ABO59722	Abc59722 Human gen	634	33	58.9	1044	9	ADW42851	Adw42851 Human cor
562	33	58.9	439	4	ABR70612	Abb70612 Drosophil	635	33	58.9	1047	7	AAO27532	Aao27532 Human pro
563	33	58.9	444	2	AAE42293	Aar42293 Cephalop	636	33	58.9	1047	7	AAO27533	Aao27533 Human HCS
564	33	58.9	449	4	ABR58423	Abb58423 Drosophil	637	33	58.9	1058	5	ABR97435	Abb97435 Novel hum
565	33	58.9	466	4	ABGL2792	Abg12792 Novel hum	638	33	58.9	1058	8	ADO19520	Ado19520 Human PRO
566	33	58.9	468	4	ABG70072	Abg70072 Human sec	639	33	58.9	1058	9	ADX06112	Adx06112 Cyclin-de
567	33	58.9	468	5	ABG65511	Abg65511 Human alb	640	33	58.9	1063	4	ABR98218	Abb98218 Human chr
568	33	58.9	468	8	ADL78778	Adl78778 Albumin f	641	33	58.9	1076	4	ABR11975	Abb11975 Human cor
569	33	58.9	475	8	ADP96783	Adp96783 Human hyp	642	33	58.9	1346	7	ABG23133	Abg23133 Novel hum
570	33	58.9	485	4	ABG22097	Abg22097 Novel hum	643	33	58.9	1514	7	ADJ69503	Adj69503 Human hea
571	33	58.9	488	4	AA95586	Aab95586 Human pro	644	33	58.9	1548	7	ADG42166	Adg42166 Human bra
572	33	58.9	488	4	ABR50231	Abb50231 Human tra	645	33	58.9	1670	5	ABR92708	Abb92708 Herbicida
573	33	58.9	488	8	ADL41459	Adl41459 Human NF-	646	33	58.9	1697	7	ADC37542	Adc37542 Human nuc
574	33	58.9	489	8	ADX74703	Adx74703 Plant ful	647	33	58.9	1931	5	ABR92232	Abb92232 Herbicida
575	33	58.9	498	3	AAV58632	Aav58632 Protein r	648	33	58.9	2006	4	ABR71277	Abb71277 Drosophil
576	33	58.9	498	7	ADP25763	Adp25763 Human pro	649	33	58.9	2006	8	ADS96448	Ads96448 Drosophil
577	33	58.9	501	2	AAE25072	Aae25072 Human t-c	650	33	58.9	3192	4	AAE10128	Aae10128 Streptomy
578	33	58.9	511	4	AAU58018	Aau58018 Propionib	651	32.5	58.0	63	4	AAU23749	Aau23749 Novel hum
579	33	58.9	511	6	ABM54537	Abm54537 Propionib	652	32.5	58.0	63	4	AAU17057	Aau17057 Human nov
580	33	58.9	514	5	ABP69474	Abp69474 Human pol	653	32.5	58.0	322	8	ADS10913	Adsl0913 Human the
581	33	58.9	520	8	ABM81692	Abm81692 Tumour-as	654	32.5	58.0	402	8	ADS10937	Adsl0937 Human the
582	33	58.9	520	9	ADV70182	Adv70182 Tumour-ass	655	32.5	58.0	472	6	ADA54710	Ada54710 Human pro
583	33	58.9	526	4	ABG04827	Abg04827 Novel hum	656	32.5	58.0	472	7	ADN95648	Adn95648 Human BEC
584	33	58.9	542	4	ABG30239	Abg30239 Novel hum	657	32.5	58.0	520	8	ADX91461	Adx91461 Plant ful
585	33	58.9	543	7	ABO69285	Abc69285 Pseudomon	658	32	57.1	9	8	ADK05628	Adk05628 Hepatitis
586	33	58.9	551	5	AAE17484	Aae17484 Human leu	659	32	57.1	43	4	AAU91623	Aau91623 Human imm
587	33	58.9	565	7	ADP08361	Adp08361 Novel pro	660	32	57.1	45	8	ADK01873	Adk01873 Hepatitis
588	33	58.9	566	5	ABP70143	Abp70143 Human NOV	661	32	57.1	47	6	ABP54179	Abp54179 Human lun
589	33	58.9	603	4	ABG03722	Abg03722 Novel hum	662	32	57.1	48	7	ADP56030	Adp56030 Human uri
590	33	58.9	618	7	ADJ21104	Adj21104 Novel hum	663	32	57.1	50	6	AAU58521	Aau58521 Propionib
591	33	58.9	626	3	AAV44502	N. crassa	664	32	57.1	50	6	AAU55040	Abm55040 Propionib
592	33	58.9	626	3	AAV44503	B. subtil	665	32	57.1	54	5	ABP01409	Abp01409 Human ORF
593	33	58.9	635	5	AAE23980	Aae23980 Human LP2	666	32	57.1	55	4	AAU91538	Aau91538 Human imm
594	33	58.9	635	6	AAO26256	AAO26256 MDDT rela	667	32	57.1	55	4	ABR14893	Abb14893 Human ner
595	33	58.9	635	9	ADZ09859	Adz09859 Human bre	668	32	57.1	59	4	ABR42071	Abb42071 Peptide #
596	33	58.9	641	4	ABG30241	Abg30241 Novel hum	669	32	57.1	59	4	AAU35872	Aau35872 Peptide #
597	33	58.9	647	5	ABP70142	Abp70142 Human NOV	670	32	57.1	61	4	ABG57502	Abg57502 Human liv
598	33	58.9	655	8	ADN19205	Adn19205 Bacterial	671	32	57.1	61	4	AAU53826	Aau53826 Propionib
599	33	58.9	656	2	AAW01618	Aaw01618 Neurospor	672	32	57.1	61	6	AAU50345	Abm50345 Propionib
600	33	58.9	665	4	ABGL1551	Abg11551 Novel hum	673	32	57.1	62	4	AAO00115	Aao00115 Human pol
601	33	58.9	667	4	ABR65676	Abb65676 Drosophil	674	32	57.1	62	4	ABP05187	Abp05187 Human ORF
602	33	58.9	685	8	ADI45303	Adi45303 Rice isop	675	32	57.1	64	4	AAU22097	Aau22097 Human car
603	33	58.9	688	6	ABR80130	E. coli b	676	32	57.1	64	7	ADW46065	Adw46065 Human car
604	33	58.9	718	1	AA91935	AA91935 Bi antigen	677	32	57.1	64	8	ADJ07483	Adj07483 Human car
605	33	58.9	719	9	ADW42858	Adw42858 Human cor	678	32	57.1	65	4	AAU54169	Aau54169 Propionib
606	33	58.9	723	5	AAU83124	Aau83124 Novel sec	679	32	57.1	65	6	ABM50688	Abm50688 Propionib
607	33	58.9	735	8	ADY22886	Ady22886 Plant ful	680	32	57.1	67	5	ADK36693	Adk36693 Novel hum
608	33	58.9	755	8	ADL18337	Adl18337 Weston mo	681	32	57.1	69	6	ABJ19727	Abj19727 Human sec

828	32	57.1	310	8	ADN26091	Bacterial	901	32	57.1	328	6	ADA95618	Human PRO
829	32	57.1	312	8	ADY08349	Plant ful	902	32	57.1	328	6	ADB25927	Human PRO
830	32	57.1	315	4	AAU508349	Propronib	903	32	57.1	328	6	ADB21412	Novel hum
831	32	57.1	315	6	ABM54776	Propronib	904	32	57.1	328	7	ADA77191	Human PRO
832	32	57.1	316	8	ADN94660	Plant ful	905	32	57.1	328	7	ADB17931	Human PRO
833	32	57.1	317	4	AAH87744	Human T2R	906	32	57.1	328	7	ADA86614	Novel hum
834	32	57.1	317	8	ADJ84507	Human T2R	907	32	57.1	328	7	ADA87717	Novel hum
835	32	57.1	317	8	ADR29087	Taste rec	908	32	57.1	328	7	ADA46105	Novel hum
836	32	57.1	317	8	ADM33327	Human bit	909	32	57.1	328	7	ADA09126	Novel hum
837	32	57.1	317	8	ADN91925	Plant ful	910	32	57.1	328	7	ADB28135	Human PRO
838	32	57.1	317	9	ADW74528	Human bit	911	32	57.1	328	7	ADB28687	Human PRO
839	32	57.1	317	9	ADW74530	Human bit	912	32	57.1	328	7	ADA76639	Human PRO
840	32	57.1	317	9	ADW74530	Human bit	913	32	57.1	328	7	ADA88269	Novel hum
841	32	57.1	317	9	ADW74526	Human bit	914	32	57.1	328	7	ADA97274	Human PRO
842	32	57.1	320	6	ADA54228	Human pro	915	32	57.1	328	7	ADB27031	Human PRO
843	32	57.1	322	4	ABR58041	Human GI	916	32	57.1	328	7	ADB21964	Novel hum
844	32	57.1	323	6	AAU67697	Propronib	917	32	57.1	328	7	ADA66655	Human PRO
845	32	57.1	323	6	ABM64216	Propronib	918	32	57.1	328	7	ADB22516	Human PRO
846	32	57.1	324	8	ADU02616	Novel hum	919	32	57.1	328	7	ADB23289	Human PRO
847	32	57.1	324	8	ADX77816	Plant ful	920	32	57.1	328	7	ADA92011	Novel hum
848	32	57.1	327	4	AAH94848	Human pro	921	32	57.1	328	7	ADB15074	Human PRO
849	32	57.1	328	4	AAU27777	Human ful	922	32	57.1	328	7	ADB38326	Novel hum
850	32	57.1	328	4	AAU12188	Human PRO	923	32	57.1	328	7	ADB37774	Novel hum
851	32	57.1	328	5	ABR05677	Human amy	924	32	57.1	328	7	ADB66246	Novel hum
852	32	57.1	328	5	ABR08213	Human car	925	32	57.1	328	7	ADB89326	Human PRO
853	32	57.1	328	5	ABR08902	Human lya	926	32	57.1	328	7	ADB90058	Human PRO
854	32	57.1	328	6	ABO17632	Novel hum	927	32	57.1	328	7	ADB39159	Novel hum
855	32	57.1	328	6	ABU80886	Human PRO	928	32	57.1	328	7	ADB46782	Novel hum
856	32	57.1	328	6	ABU66586	Human PRO	929	32	57.1	328	7	ADB86389	Human PRO
857	32	57.1	328	6	ABU59667	Novel sec	930	32	57.1	328	7	ADB76994	Novel hum
858	32	57.1	328	6	ABO24857	Human sec	931	32	57.1	328	7	ADB34151	Human PRO
859	32	57.1	328	6	ADA66862	Human sec	932	32	57.1	328	7	ADB35255	Human PRO
860	32	57.1	328	6	ADA45553	Novel hum	933	32	57.1	328	7	ADB33599	Human PRO
861	32	57.1	328	6	ADA75984	Human PRO	934	32	57.1	328	7	ADB34703	Human PRO
862	32	57.1	328	6	ADA18634	Human PRO	935	32	57.1	328	7	ADB35807	Human PRO
863	32	57.1	328	6	ADA61257	Homo sapi	936	32	57.1	328	7	ADB46202	Novel hum
864	32	57.1	328	6	ADB19042	Novel hum	937	32	57.1	328	7	ADC50075	Novel hum
865	32	57.1	328	6	ADB27583	Human PRO	938	32	57.1	328	7	ADC71622	Novel hum
866	32	57.1	328	6	ADA86062	Novel hum	939	32	57.1	328	7	ADC59601	Novel hum
867	32	57.1	328	6	ADB15626	Human PRO	940	32	57.1	328	7	ADC52608	Novel hum
868	32	57.1	328	6	ADA47412	Human PRO	941	32	57.1	328	7	ADC56962	Novel hum
869	32	57.1	328	6	ADA67207	Human PRO	942	32	57.1	328	7	ADC60153	Novel hum
870	32	57.1	328	6	ADB30214	Human PRO	943	32	57.1	328	7	ADC50628	Novel hum
871	32	57.1	328	6	ADA85510	Novel hum	944	32	57.1	328	7	ADC65155	Human PRO
872	32	57.1	328	6	ADA96722	Human PRO	945	32	57.1	328	7	ADC54253	Novel hum
873	32	57.1	328	6	ADA79026	Human PRO	946	32	57.1	328	7	ADC53214	Novel hum
874	32	57.1	328	6	ADA87165	Novel hum	947	32	57.1	328	7	ADC58737	Novel hum
875	32	57.1	328	6	ADB16367	Human PRO	948	32	57.1	328	7	ADC55615	Novel hum
876	32	57.1	328	6	ADA91459	Novel hum	949	32	57.1	328	7	ADC58185	Novel hum
877	32	57.1	328	6	ADB14522	Human PRO	950	32	57.1	328	7	ADC02859	Novel hum
878	32	57.1	328	6	ADB18483	Novel hum	951	32	57.1	328	7	ADC89851	Novel hum
879	32	57.1	328	6	ADA93698	Human PRO	952	32	57.1	328	7	ADC69270	Human PRO
880	32	57.1	328	6	ADB19594	Novel hum	953	32	57.1	328	7	ADC48159	Human PRO
881	32	57.1	328	6	ADB12906	Human PRO	954	32	57.1	328	7	ADC09688	Human PRO
882	32	57.1	328	6	ABO43165	Novel hum	955	32	57.1	328	7	ADC04263	Novel hum
883	32	57.1	328	6	ADA74160	Human PRO	956	32	57.1	328	7	ADC80219	Novel hum
884	32	57.1	328	6	ADB24393	Human PRO	957	32	57.1	328	7	ADC10726	Novel hum
885	32	57.1	328	6	ADA81917	Human PRO	958	32	57.1	328	7	ADC47607	Human PRO
886	32	57.1	328	6	ADA74880	Human PRO	959	32	57.1	328	7	ADC79667	Novel hum
887	32	57.1	328	6	ADA84958	Novel hum	960	32	57.1	328	7	ADC09136	Human PRO
888	32	57.1	328	6	ADA84406	Novel hum	961	32	57.1	328	7	ADA40849	Novel hum
889	32	57.1	328	6	ADB29662	Human PRO	962	32	57.1	328	7	ADC51988	Novel hum
890	32	57.1	328	6	ADA80190	Human PRO	963	32	57.1	328	7	ADC52728	Human PRO
891	32	57.1	328	6	ADA75432	Human PRO	964	32	57.1	328	7	ADC53280	Novel hum
892	32	57.1	328	6	ADA46657	Human PRO	965	32	57.1	328	7	ADC51436	Human PRO
893	32	57.1	328	6	ADB24953	Human PRO	966	32	57.1	328	7	ADC02235	Human PRO
894	32	57.1	328	6	ADA93129	Human PRO	967	32	57.1	328	7	ADC01669	Human PRO
895	32	57.1	328	6	ADB26479	Human PRO	968	32	57.1	328	7	ADC53851	Novel hum
896	32	57.1	328	6	ADB30766	Human PRO	969	32	57.1	328	7	ADC92168	Human PRO
897	32	57.1	328	6	ADA60694	Homo sapi	970	32	57.1	328	7	ADC91064	Human PRO
898	32	57.1	328	6	ADB23841	Human PRO	971	32	57.1	328	7	ADC03678	Human PRO
899	32	57.1	328	6	ADA96170	Human PRO	972	32	57.1	328	7	ADC31975	Novel hum
900	32	57.1	328	6	ADA80742	Human PRO	973	32	57.1	328	7	ADC21907	Human PRO

974 32 57.1 328 7 ADD79131 Human PRO
 975 32 57.1 328 7 ADE41667 Human PRO
 976 32 57.1 328 7 ADE17484 Human PRO
 977 32 57.1 328 7 ADD91616 Human PRO
 978 32 57.1 328 7 ADE33079 Novel hum
 979 32 57.1 328 7 ADE33631 Novel hum
 980 32 57.1 328 7 ADD79683 Human PRO
 981 32 57.1 328 7 ADD92720 Human PRO
 982 32 57.1 328 7 ADE19140 Human PRO
 983 32 57.1 328 7 ADE18588 Human PRO
 984 32 57.1 328 7 ADE42784 Human PRO
 985 32 57.1 328 7 ADD95573 Human PRO
 986 32 57.1 328 7 ADE22459 Human PRO
 987 32 57.1 328 7 ADD78577 Human PRO
 988 32 57.1 328 7 ADE32527 Novel hum
 989 32 57.1 328 7 ADE42219 Human PRO
 990 32 57.1 328 7 ADD80235 Human PRO
 991 32 57.1 328 7 ADD89263 Human PRO
 992 32 57.1 328 7 ADE40547 Human PRO
 993 32 57.1 328 7 ADE04346 Human PRO
 994 32 57.1 328 7 ADE92475 Human PRO
 995 32 57.1 328 7 ADG21184 Novel hum
 996 32 57.1 328 7 ADG22825 Novel hum
 997 32 57.1 328 7 ADE97160 Human PRO
 998 32 57.1 328 7 ADG80224 Human PRO
 999 32 57.1 328 7 ADG79672 Human PRO
 1000 32 57.1 328 7 ADH54964 Novel hum

ALIGNMENTS

RESULT 1
 ADI15844
 ID ADI15844 standard; peptide; 10 AA.
 AC ADI15844;
 XX
 XX
 XX
 XX 22-APR-2004 (first entry)
 DE HLA-A2 restricted cytotoxic T lymphocyte recognised peptide #187.
 DE tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;
 KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;
 KW stomach cancer; buccal cancer; renal cancer; lung cancer;
 KW gynecological cancer; prostate cancer.
 XX
 OS Synthetic.
 XX
 XX WO2003008450-A1.
 XX
 XX 30-JAN-2003.
 XX
 XX 11-JUN-2002; 2002WO-JP005799.
 XX
 XX 12-JUN-2001; 2001JP-00177058.
 PR 21-AUG-2001; 2001JP-00250728.
 XX
 XX (ITOH/) ITOH K.
 PA
 XX
 XX Itoh K, Shichiho S;
 XX
 XX WPI; 2003-267996/26.
 XX
 XX Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or
 PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of
 PT cancer including preparation of cancer vaccines.
 XX
 PS Claim 1; SEQ ID NO 188; 323pp; Japanese.
 XX
 XX The invention relates to a tumour antigen peptide recognised by human
 CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)
 CC and/or capable of inducing CTL. The tumour antigen peptide is useful for

CC the treatment, prevention, diagnosis and vaccine production for cancers
 CC including colorectal, stomach, buccal, renal, lung, gynecological and
 CC prostate cancer. The present sequence represents a peptide recognised by
 CC HLA-A2 restricted cytotoxic T lymphocytes.
 XX
 SQ Sequence 10 AA;

Query Match Similarity 100.0%; Score 56; DB 7; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LMALPPCHAL 10

Db 1 LMALPPCHAL 10

RESULT 2

ID ABG20769 standard; protein; 216 AA.

XX ABG20769;

AC ABG20769;

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #20760.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00849167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS84956.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 51128; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 216 AA;

Query Match 100.0%; Score 56; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
|||
Db 116 LMALPPCHAL 125

RESULT 3

ADC56779
ID ADC56779 standard; protein; 230 AA.

XX
AC ADC56779;

XX 18-DEC-2003 (first entry)

XX Splice variant 1 of human thymidyllic acid synthetase protein.

XX human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.

XX Homo sapiens.

XX JP2003102480-A.

XX 08-APR-2003.

XX 28-SEP-2001; 2001JP-00300086.

XX 28-SEP-2001; 2001JP-00300086.

XX (SRLS-) SRL KK.

XX WPI; 2003-649087/62.

XX N-PSDB; ADC56767.

XX Measuring human thymidyllic-acid synthetase mRNA, by using primers that
PT hybridize to full length cDNA of thymidyllic-acid synthetase gene but does
PT not hybridize to variant cDNA in which specific exons of gene are
PT deleted.

XX Disclosure; Page 20-21; 28pp; Japanese.

XX This invention relates to a novel method for measuring human thymidyllic
CC acid synthetase (hts) mRNA (EC 2.1.1.45). Specifically, it comprises
CC amplifying cDNA or mRNA of the hts gene using forward and reverse
CC primers, where the forward primer does not hybridize to the variant cDNA
CC in which exon 2 and exon 3 of the gene are deleted. Likewise the reverse
CC primer does not hybridize to the variant cDNA in which exon 4 of the hts
CC gene has been deleted. Accordingly, by measuring the amplified product of
CC human thymidyllic acid synthetase it is possible to exactly measure only
CC the active hts enzyme product, which is useful in the prognosis or
CC treatment of cancer. Furthermore, the throughput of hts in a cancer cell
CC can estimate the therapeutic effect of an anticancer agent. This
CC polypeptide sequence is the splice variant 1 of human thymidyllic acid
CC synthetase protein of the invention. NOTE: This protein is not further
CC described in the specification but is given as an embedded protein in
CC the sequence listing.

XX Sequence 230 AA;

Query Match 100.0%; Score 56; DB 7; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

Db 106 LMALPPCHAL 115

RESULT 4

ADC56780

ID ADC56780 standard; protein; 279 AA.

XX
AC ADC56780;

XX 18-DEC-2003 (first entry)

XX Splice variant 2 of human thymidyllic acid synthetase protein.

XX human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.

XX Homo sapiens.

XX JP2003102480-A.

XX 08-APR-2003.

XX 28-SEP-2001; 2001JP-00300086.

XX 28-SEP-2001; 2001JP-00300086.

XX (SRLS-) SRL KK.

XX WPI; 2003-649087/62.

XX N-PSDB; ADC56768.

XX Measuring human thymidyllic-acid synthetase mRNA, by using primers that
PT hybridize to full length cDNA of thymidyllic-acid synthetase gene but does
PT not hybridize to variant cDNA in which specific exons of gene are
PT deleted.

XX Disclosure; Page 22-23; 28pp; Japanese.

XX This invention relates to a novel method for measuring human thymidyllic
CC acid synthetase (hts) mRNA (EC 2.1.1.45). Specifically, it comprises
CC amplifying cDNA or mRNA of the hts gene using forward and reverse
CC primers, where the forward primer does not hybridize to the variant cDNA
CC in which exon 2 and exon 3 of the gene are deleted. Likewise the reverse
CC primer does not hybridize to the variant cDNA in which exon 4 of the hts
CC gene has been deleted. Accordingly, by measuring the amplified product of
CC human thymidyllic acid synthetase it is possible to exactly measure only
CC the active hts enzyme product, which is useful in the prognosis or
CC treatment of cancer. Furthermore, the throughput of hts in a cancer cell
CC can estimate the therapeutic effect of an anticancer agent. This
CC polypeptide sequence is the splice variant 2 of human thymidyllic acid
CC synthetase protein of the invention. NOTE: This protein is not further
CC described in the specification but is given as an embedded protein in
CC the sequence listing.

XX Sequence 279 AA;

Query Match 100.0%; Score 56; DB 7; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

Db 155 LMALPPCHAL 164

RESULT 5

ABP53743

ID ABP53743 standard; protein; 284 AA.

XX
AC ABP53743;

XX 02-JAN-2003 (first entry)

XX Human thymidylate synthase amino acid sequence.

XX

Thymidylate synthase; enzyme; binding; neoplastic disorder;
chemotherapeutic; cytostatic; thymidylate synthase inhibitor; cancer.

Homo sapiens.

Key Location/Qualifiers
Peptide 31..47
/label= Peptide 9
/note= "thymidylate synthase binding peptide"
Peptide 56..72
/label= Peptide 14
/note= "thymidylate synthase binding peptide"
Peptide 131..147
/label= Peptide 29
/note= "thymidylate synthase binding peptide"
Peptide 175..192
/label= Peptide 38
/note= "thymidylate synthase binding peptide"
Peptide 201..217
/label= Peptide 43
/note= "thymidylate synthase binding peptide"

WO200272753-A2.

19-SEP-2002.

05-MAR-2002; 2002WO-US006634.

07-MAR-2001; 2001US-0274107P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Allegra CJ, Voeller DM;

WPI; 2002-732823/79.

New isolated peptide binding to an mRNA encoding thymidylate synthase,
useful for treating and/or diagnosing disorders such as cancer of a head
and neck, breast, prostate, liver, lung, gastric, colon or esophagus.

Example 2; Fig 1B; 59pp; English.

The present invention describes a peptide (I) which binds to an mRNA
encoding a thymidylate synthase (TS) polypeptide. Also described: (1)
inhibiting translation of a mRNA encoding TS comprising contacting the
mRNA, or a cell expressing the mRNA with a peptide comprising 10-25
consecutive amino acids of the peptide interface region of the TS, where
the peptide binds to the mRNA encoding TS, and inhibits the translation
of the mRNA encoding TS; and (2) treating a subject with a neoplastic
disorder comprising administering to the subject a chemotherapeutic agent
and a TS peptide or a therapeutic nucleic acid sequence comprising a
promoter operably linked to a nucleic acid sequence encoding TS peptide
that comprises 10-25 amino acids of the peptide interface region of the
TS, where the peptide binds to the mRNA encoding TS, and inhibits the
translation of the mRNA encoding TS, treating the neoplastic disorder.
(I) has cytostatic activity, and can be used as a TS inhibitor. The
methods and compositions of the present invention are useful for treating
and/or diagnosing disorders associated with the TS peptide, such as
cancer of a head and neck, breast, prostate, liver, lung, gastric, colon
or oesophagus. They are also used to enhance the effect of other
chemotherapeutic agents. The present sequence represents a human
thymidylate synthase amino acid sequence, which is used in an example
from the present invention

Sequence 284 AA;

Query Match 100.0%; Score 56; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
|
Db 189 LMALPPCHAL 198

RESULT 6

AAW75754
ID AAW75754 standard; protein; 313 AA.

AC AAW75754;

DT 19-NOV-1998 (first entry)

DE Mutated thymidylate synthase.

XX Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3bTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 52

FT /note= "Wild-type Gly substituted by Ser"

XX WO9833518-A1.

PD 06-AUG-1998.

XX 03-FEB-1998; 98WO-US002145.

XX 04-FEB-1997; 97US-0037163P.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Bertino JR, Tong Y, Liu-Chen X, Banerjee D;

XX WPI; 1998-437173/37.

XX New mutant human thymidylate synthases - used to, e.g. develop products
FT for use in gene therapy and for treating cancers.

PS Claim 3; Page; 78pp; English.

XX Sequences AAW75752-W5768 represent thymidylate synthase (TS) mutants
most of which were generated by using site directed mutagenesis. This was
performed by creating a TS expression vector pCDNA3bTS which contained
the human TS gene coding sequence, and using this to produce ssDNA for
site-directed mutagenesis and sequence analysis. Mutants which were not
created this way were produced by random mutagenesis, by exposing human
sarcoma HT1080 cells to an alkylating agent and then using AG337 for
selection. From these mutagenesis experiments, 17 different mutants were
obtained, each of which were mutated at one of five different amino acid
positions causing an amino acid change and thus causing the TS enzyme to
have different properties. It was found that mutations at positions 49
and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
mutations at 108 were found to confer tomudex and AG337 resistance. In
general mutated TS cDNAs have been found to be resistant to TS specific
inhibitors, and to have a high catalytic efficiency and good stability.
The mutant TS cDNA can be used in gene therapy to transfer drug
resistance to human haematopoietic progenitors, thus allowing dose-
intense therapy in cancer patients by protecting normal cells and
preventing dose-limiting myelotoxicity. N.B. The present sequence is not
shown in the specification but was derived from the TS wild-type
sequence, also not given in the specification

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPCHAL 10
|
Db 189 LMALPPCHAL 198

RESULT 7

AAW75758
ID AAW75758 standard; protein; 313 AA.
XX
AC AAW75758;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 108
FT Misc-difference /note= "Wild-type Ile substituted by Glu"
XX
PN WO98333518-Al.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
DR WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 4; Page; 78pp; English.

Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants most of which were generated by using site directed mutagenesis. This was performed by creating a TS expression vector pCDNA3hTS which contained the human TS gene coding sequence, and using this to produce ssDNA for site-directed mutagenesis and sequence analysis. Mutants which were not created this way were produced by random mutagenesis, by exposing human sarcoma HT1080 cells to an alkylating agent and then using AG337 for selection. From these mutagenesis experiments, 17 different mutants were obtained, each of which were mutated at one of five different amino acid positions causing an amino acid change and thus causing the TS enzyme to have different properties. It was found that mutations at positions 49 and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas mutations at 108 were found to confer tomudex and AG337 resistance. In general mutated TS cDNAs have been found to be resistant to TS specific inhibitors, and to have a high catalytic efficiency and good stability. The mutant TS cDNA can be used in gene therapy to transfer drug resistance to human haematopoietic progenitors, thus allowing dose-intense therapy in cancer patients by protecting normal cells and preventing dose-limiting myelotoxicity. N.B. The present sequence is not shown in the specification but was derived from the TS wild-type sequence, also not given in the specification

SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

DB 189 LMALPPCHAL 198

RESULT 8

AAW75765
ID AAW75765 standard; protein; 313 AA.
XX
AC AAW75765;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 225
FT Misc-difference /note= "Wild-type Phe substituted by Trp"
XX
PN WO98333518-Al.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
DR WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 6; Page; 78pp; English.

Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants most of which were generated by using site directed mutagenesis. This was performed by creating a TS expression vector pCDNA3hTS which contained the human TS gene coding sequence, and using this to produce ssDNA for site-directed mutagenesis and sequence analysis. Mutants which were not created this way were produced by random mutagenesis, by exposing human sarcoma HT1080 cells to an alkylating agent and then using AG337 for selection. From these mutagenesis experiments, 17 different mutants were obtained, each of which were mutated at one of five different amino acid positions causing an amino acid change and thus causing the TS enzyme to have different properties. It was found that mutations at positions 49 and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas mutations at 108 were found to confer tomudex and AG337 resistance. In general mutated TS cDNAs have been found to be resistant to TS specific inhibitors, and to have a high catalytic efficiency and good stability. The mutant TS cDNA can be used in gene therapy to transfer drug resistance to human haematopoietic progenitors, thus allowing dose-intense therapy in cancer patients by protecting normal cells and preventing dose-limiting myelotoxicity. N.B. The present sequence is not shown in the specification but was derived from the TS wild-type sequence, also not given in the specification

SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

DB 189 LMALPPCHAL 198

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RESULT 9
AAW75757
ID AAW75757 standard; protein; 313 AA.
XX
AC AAW75757;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 108 /note= "Wild-type Ile substituted by Gly"
FT
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
PI WPI; 1998-437173/37.
XX
DR
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 4; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198
|||||
|||||

RESULT 10
AAW75766
ID AAW75766 standard; protein; 313 AA.
XX
AC AAW75766;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 225 /note= "Wild-type Phe substituted by Ser"
FT
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
PI WPI; 1998-437173/37.
XX
DR
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 6; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198
|||||
|||||
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RESULT 11
AAW75752
ID AAW75752 standard; protein; 313 AA.
XX AC AAW75752;
XX DT 19-NOV-1998 (first entry)
XX DE Mutated thymidylate synthase.
XX KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hTS;
XX KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
XX KW tomudex; gene therapy; cancer; myelotoxicity.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 49 /note= "Wild-type Asp substituted by Asn"
XX FT
XX PN WO9833518-A1.
XX PD 06-AUG-1998.
XX PF 03-FEB-1998; 98WO-US002145.
XX PR 04-FEB-1997; 97US-0037163P.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX DR WPI; 1998-437173/37.
XX PT New mutant human thymidylate synthases - used to, e.g. develop products
XX PT for use in gene therapy and for treating cancers.
XX PS Claim 2; Page; 78pp; English.
XX CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3hTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

RESULT 12
AAW75763
ID AAW75763 standard; protein; 313 AA.
XX AC AAW75763;
XX DT 19-NOV-1998 (first entry)
XX DE Mutated thymidylate synthase.
XX KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3hTS;
XX KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
XX KW tomudex; gene therapy; cancer; myelotoxicity.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 221 /note= "Wild-type Leu substituted by Ile"
XX FT
XX PN WO9833518-A1.
XX PD 06-AUG-1998.
XX PF 03-FEB-1998; 98WO-US002145.
XX PR 04-FEB-1997; 97US-0037163P.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX DR WPI; 1998-437173/37.
XX PT New mutant human thymidylate synthases - used to, e.g. develop products
XX PT for use in gene therapy and for treating cancers.
XX PS Claim 5; Page; 78pp; English.
XX CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3hTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

```

RESULT 13
AAW75764
ID AAW75764 standard; protein; 313 AA.
XX
AC AAW75764;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 221
FT /note= "Wild-type Leu substituted by Ser"
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
DR WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 5; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pCDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

RESULT 14
AAW75755
ID AAW75755 standard; protein; 313 AA.
XX
AC AAW75755;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 108
FT /note= "Wild-type Ile substituted by Ala"
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
DR WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 4; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pCDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

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RESULT 15

AAW75768
ID AAW75768 standard; protein; 313 AA.

XX AC AAW75768;

XX DT 19-NOV-1998 (first entry)

XX DE Mutated thymidylate synthase.

XX KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hts;
XX random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
XX tomudex; gene therapy; cancer; myelotoxicity.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 225 /note= "Wild-type Phe substituted by Tyr"

XX PN WO9833518-Al.

XX PD 06-AUG-1998.

XX PF 03-FEB-1998; 98WO-US002145.

XX PR 04-FEB-1997; 97US-0037163P.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;

XX DR WPI; 1998-437173/37.

XX PT New mutant human thymidylate synthases - used to, e.g. develop products
XX for use in gene therapy and for treating cancers.

XX PS Claim 6; Page; 78pp; English.

XX CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
XX most of which were generated by using site directed mutagenesis. This was
XX performed by creating a TS expression vector pCDNA3hts which contained
XX the human TS gene coding sequence, and using this to produce ssDNA for
XX site-directed mutagenesis and sequence analysis. Mutants which were not
XX created this way were produced by random mutagenesis, by exposing human
XX sarcoma HT1080 cells to an alkylating agent and then using AG337 for
XX selection. From these mutagenesis experiments, 17 different mutants were
XX obtained, each of which were mutated at one of five different amino acid
XX positions causing an amino acid change and thus causing the TS enzyme to
XX have different properties. It was found that mutations at positions 49
XX and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
XX mutations at 108 were found to confer tomudex and AG337 resistance. In
XX general mutated TS cDNAs have been found to be resistant to TS specific
XX inhibitors, and to have a high catalytic efficiency and good stability.
XX The mutant TS cDNA can be used in gene therapy to transfer drug

XX resistance to human haematopoietic progenitors, thus allowing dose-
XX intense therapy in cancer patients by protecting normal cells and
XX preventing dose-limiting myelotoxicity. N.B. The present sequence is not
XX shown in the specification but was derived from the TS wild-type
XX sequence, also not given in the specification

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

DB 189 LMALPPCHAL 198

RESULT 16

AAW75762
ID AAW75762 standard; protein; 313 AA.

XX AC AAW75762;

XX DT 19-NOV-1998 (first entry)

XX DE Mutated thymidylate synthase.

XX KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pCDNA3hts;
XX random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
XX tomudex; gene therapy; cancer; myelotoxicity.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 221 /note= "Wild-type Leu substituted by Ala"

XX PN WO9833518-Al.

XX PD 06-AUG-1998.

XX PF 03-FEB-1998; 98WO-US002145.

XX PR 04-FEB-1997; 97US-0037163P.

XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;

XX DR WPI; 1998-437173/37.

XX PT New mutant human thymidylate synthases - used to, e.g. develop products
XX for use in gene therapy and for treating cancers.

XX PS Claim 5; Page; 78pp; English.

XX CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
XX most of which were generated by using site directed mutagenesis. This was
XX performed by creating a TS expression vector pCDNA3hts which contained
XX the human TS gene coding sequence, and using this to produce ssDNA for
XX site-directed mutagenesis and sequence analysis. Mutants which were not
XX created this way were produced by random mutagenesis, by exposing human
XX sarcoma HT1080 cells to an alkylating agent and then using AG337 for
XX selection. From these mutagenesis experiments, 17 different mutants were
XX obtained, each of which were mutated at one of five different amino acid
XX positions causing an amino acid change and thus causing the TS enzyme to
XX have different properties. It was found that mutations at positions 49
XX and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
XX mutations at 108 were found to confer tomudex and AG337 resistance. In
XX general mutated TS cDNAs have been found to be resistant to TS specific
XX inhibitors, and to have a high catalytic efficiency and good stability.
XX The mutant TS cDNA can be used in gene therapy to transfer drug

XX resistance to human haematopoietic progenitors, thus allowing dose-
XX intense therapy in cancer patients by protecting normal cells and
XX preventing dose-limiting myelotoxicity. N.B. The present sequence is not
XX shown in the specification but was derived from the TS wild-type
XX sequence, also not given in the specification

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

DB 189 LMALPPCHAL 198

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RESULT 17
AAW75756
ID AAW75756 standard; protein; 313 AA.
XX
AC AAW75756;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 108
FT /note= "Wild-type Ile substituted by Phe"
XX
XX WO9833518-A1.
XX
XX 06-AUG-1998.
XX
XX 03-FEB-1998; 98WO-US002145.
XX
XX 04-FEB-1997; 97US-0037163P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX WPI; 1998-437173/37.
XX
XX New mutant human thymidylate synthases - used to, e.g. develop products
XX for use in gene therapy and for treating cancers.
XX
XX Claim 4; Page; 78pp; English.
XX
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
XX most of which were generated by using site directed mutagenesis. This was
XX performed by creating a TS expression vector pcDNA3HTS which contained
XX the human TS gene coding sequence, and using this to produce ssDNA for
XX site-directed mutagenesis and sequence analysis. Mutants which were not
XX created this way were produced by random mutagenesis, by exposing human
XX sarcoma HT1080 cells to an alkylating agent and then using AG337 for
XX selection. From these mutagenesis experiments, 17 different mutants were
XX obtained, each of which were mutated at one of five different amino acid
XX positions causing an amino acid change and thus causing the TS enzyme to
XX have different properties. It was found that mutations at positions 49
XX and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
XX mutations at 108 were found to confer tomudex and AG337 resistance. In
XX general mutated TS cDNAs have been found to be resistant to TS specific
XX inhibitors, and to have a high catalytic efficiency and good stability.
XX The mutant TS cDNA can be used in gene therapy to transfer drug
XX resistance to human haematopoietic progenitors, thus allowing dose-
XX intense therapy in cancer patients by protecting normal cells and
XX preventing dose-limiting myelotoxicity. N.B. The present sequence is not
XX shown in the specification but was derived from the TS wild-type
XX sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

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RESULT 18
AAW75759
ID AAW75759 standard; protein; 313 AA.
XX
AC AAW75759;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 108
FT /note= "Wild-type Ile substituted by Asn"
XX
XX WO9833518-A1.
XX
XX 06-AUG-1998.
XX
XX 03-FEB-1998; 98WO-US002145.
XX
XX 04-FEB-1997; 97US-0037163P.
XX
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
XX Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX WPI; 1998-437173/37.
XX
XX New mutant human thymidylate synthases - used to, e.g. develop products
XX for use in gene therapy and for treating cancers.
XX
XX Claim 4; Page; 78pp; English.
XX
XX Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
XX most of which were generated by using site directed mutagenesis. This was
XX performed by creating a TS expression vector pcDNA3HTS which contained
XX the human TS gene coding sequence, and using this to produce ssDNA for
XX site-directed mutagenesis and sequence analysis. Mutants which were not
XX created this way were produced by random mutagenesis, by exposing human
XX sarcoma HT1080 cells to an alkylating agent and then using AG337 for
XX selection. From these mutagenesis experiments, 17 different mutants were
XX obtained, each of which were mutated at one of five different amino acid
XX positions causing an amino acid change and thus causing the TS enzyme to
XX have different properties. It was found that mutations at positions 49
XX and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
XX mutations at 108 were found to confer tomudex and AG337 resistance. In
XX general mutated TS cDNAs have been found to be resistant to TS specific
XX inhibitors, and to have a high catalytic efficiency and good stability.
XX The mutant TS cDNA can be used in gene therapy to transfer drug
XX resistance to human haematopoietic progenitors, thus allowing dose-
XX intense therapy in cancer patients by protecting normal cells and
XX preventing dose-limiting myelotoxicity. N.B. The present sequence is not
XX shown in the specification but was derived from the TS wild-type
XX sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

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RESULT 19
AAW75767
ID AAW75767 standard; protein; 313 AA.
XX
AC AAW75767;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcdNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 225
FT /note= "Wild-type Phe substituted by Leu"
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
XX WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 6; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcdNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. NO. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMAALPPCHAL 10
DB 189 LMAALPPCHAL 198

RESULT 20
AAW75760
ID AAW75760 standard; protein; 313 AA.
XX
AC AAW75760;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcdNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 221
FT /note= "Wild-type Leu substituted by Phe"
XX
PN WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
XX WPI; 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 5; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcdNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. NO. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMAALPPCHAL 10
DB 189 LMAALPPCHAL 198

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RESULT 21
AAW75761
ID AAW75761 standard; protein; 313 AA.
XX
AC AAW75761;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 221 /note= "Wild-type Leu substituted by Arg"
FT
XX WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
WPI; 1998-437173/37.
XX
DR New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 5; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

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RESULT 22
AAW75753
ID AAW75753 standard; protein; 313 AA.
XX
AC AAW75753;
XX
DT 19-NOV-1998 (first entry)
XX
DE Mutated thymidylate synthase.
XX
KW Mutation; thymidylate synthase; TS; site directed mutagenesis; pcDNA3HTS;
KW random mutagenesis; sarcoma HT1080 cell; alkylating agent; AG337; FdUrd;
KW tomudex; gene therapy; cancer; myelotoxicity.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 49 /note= "Wild-type Asp substituted by Gly"
FT
XX WO9833518-A1.
XX
PD 06-AUG-1998.
XX
PF 03-FEB-1998; 98WO-US002145.
XX
PR 04-FEB-1997; 97US-0037163P.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Bertino JR, Tong Y, Liu-Chen X, Banerjee D;
XX
WPI; 1998-437173/37.
XX
DR New mutant human thymidylate synthases - used to, e.g. develop products
PT for use in gene therapy and for treating cancers.
XX
PS Claim 2; Page; 78pp; English.
XX
CC Sequences AAW75752-W75768 represent thymidylate synthase (TS) mutants
CC most of which were generated by using site directed mutagenesis. This was
CC performed by creating a TS expression vector pcDNA3HTS which contained
CC the human TS gene coding sequence, and using this to produce ssDNA for
CC site-directed mutagenesis and sequence analysis. Mutants which were not
CC created this way were produced by random mutagenesis, by exposing human
CC sarcoma HT1080 cells to an alkylating agent and then using AG337 for
CC selection. From these mutagenesis experiments, 17 different mutants were
CC obtained, each of which were mutated at one of five different amino acid
CC positions causing an amino acid change and thus causing the TS enzyme to
CC have different properties. It was found that mutations at positions 49
CC and 52 caused the enzyme to form resistance to AG337 and FdUrd, whereas
CC mutations at 108 were found to confer tomudex and AG337 resistance. In
CC general mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing dose-
CC intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity. N.B. The present sequence is not
CC shown in the specification but was derived from the TS wild-type
CC sequence, also not given in the specification
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198

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RESULT 23
 ABP53744
 ID ABP53744 standard; protein; 313 AA.
 XX AC ABP53744;
 XX DT 02-JAN-2003 (first entry)
 XX DE Human thymidylate synthase SEQ ID NO:14.
 XX KW Thymidylate synthase; enzyme; binding; neoplastic disorder;
 XX KW chemotherapeutic; cytostatic; thymidylate synthase inhibitor; cancer.
 XX OS Homo sapiens.
 XX PN WO200272753-A2.
 XX PD 19-SEP-2002.
 XX PF 05-MAR-2002; 2002WO-US006634.
 XX PR 07-MAR-2001; 2001US-0274107P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Allegra CJ, Voeller DM;
 XX WPI: 2002-732823/79.
 XX N-PSDB; ABQ82701.
 XX New isolated peptide binding to an mRNA encoding thymidylate synthase,
 PT useful for treating and/or diagnosing disorders such as cancer of a head
 PT and neck, breast, prostate, liver, lung, gastric, colon or esophagus.
 XX Claim 6; Fig 2B; 59pp; English.
 XX The present invention describes a peptide (I) which binds to an mRNA
 CC encoding a thymidylate synthase (TS) polypeptide. Also described: (1)
 CC inhibiting translation of a mRNA encoding TS comprising contacting the
 CC mRNA, or a cell expressing the mRNA with a peptide comprising 10-25
 CC consecutive amino acids of the peptide interface region of the TS, where
 CC the peptide binds to the mRNA encoding TS, and inhibits the translation
 CC of the mRNA encoding TS; and (2) treating a subject with a neoplastic
 CC disorder comprising administering to the subject a chemotherapeutic agent
 CC and a TS peptide or a therapeutic nucleic acid sequence comprising a
 CC promoter operably linked to a nucleic acid sequence encoding TS peptide
 CC that comprises 10-25 amino acids of the peptide interface region of the
 CC TS, where the peptide binds to the mRNA encoding TS, and inhibits the
 CC translation of the mRNA encoding TS, treating the neoplastic disorder.
 CC (I) has cytostatic activity, and can be used as a TS inhibitor. The
 CC methods and compositions of the present invention are useful for treating
 CC and/or diagnosing disorders associated with the TS peptide, such as
 CC cancer of a head and neck, breast, prostate, liver, lung, gastric, colon
 CC or esophagus. They are also used to enhance the effect of other
 CC chemotherapeutic agents. The present sequence represents human
 CC thymidylate synthase, which is used in an example from the present
 CC invention
 XX Sequence 313 AA;
 SQ Query Match 100.0%; Score 56; DB 5; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 189 LMALPPCHAL 198
 RESULT 24
 AAU87071
 ID AAU87071 standard; protein; 313 AA.
 XX AC AAU87071;
 XX DT 05-JUN-2002 (first entry)
 XX DE Human thymidylate synthase.
 XX KW HKNG1; chromosome 18p; bipolar affective disorder; BAD;
 XX KW severe bipolar affective (mood) disorder; BP-I; schizophrenia; TS;
 XX KW Hong Kong new gene 1; antimanic; antidepressant; neuroleptic;
 XX KW Thymidylate synthase.
 XX OS Homo sapiens.
 XX PN WO200210366-A2.
 XX PD 07-FEB-2002.
 XX PF 02-AUG-2001; 2001WO-US024417.
 XX PR 02-AUG-2000; 2000US-00631275.
 XX PR 28-NOV-2000; 2000US-00722544.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chen H, Freimer NB, Novak T;
 XX WPI: 2002-195962/25.
 XX N-PSDB; ABR43335.
 XX New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
 PT screening for molecules which modulate HKNG1 expression for the treatment
 PT of bipolar disorder and schizophrenia.
 XX Disclosure; Fig 45; 367pp; English.
 XX The invention relates to an isolated nucleic acid molecule comprising a
 CC nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
 CC product. The human gene for HKNG1 is located on chromosome 18p in an area
 CC associated with bipolar affective disorder. BAD. Also included are an
 CC expression vector comprising the nucleic acid, a host cell expressing the
 CC nucleic acid, an anti-HKNG1 antibody, a method of identifying modulators
 CC of HKNG1, and identifying an individual (at risk of) having HKNG1-
 CC mediated disorder comprising detecting the presence or absence of a
 CC polymorphism that correlates with an HKNG1 allele associated with the
 CC disorder, where the presence of the polymorphism indicates that the
 CC individual (is at risk of) having HKNG1-mediated disorder. A (small
 CC molecule) compound which modulates (inhibits or potentiates) expression
 CC of a HKNG1 gene or gene product in a human individual is useful for the
 CC treatment of a HKNG1-mediated disorder such as bipolar affective disorder
 CC (BAD), severe bipolar affective (mood) disorder (BP-I) and schizophrenia.
 CC The present sequence is the thymidylate synthase, TS, protein. The gene
 CC for TS overlaps that of HKNG1 and therefore TS may also be involved in
 CC the diseases listed above
 XX Sequence 313 AA;
 SQ Query Match 100.0%; Score 56; DB 5; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 189 LMALPPCHAL 198
 RESULT 25
 ADC56778
 ID ADC56778 standard; protein; 313 AA.
 XX AC ADC56778;
 XX

DT 18-DEC-2003 (first entry)
 XX Human thymidyllic acid synthetase protein.
 DE human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.
 XX human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.
 KW Homo sapiens.
 OS JP2003102480-A.
 XX 08-APR-2003.
 XX 28-SEP-2001; 2001JP-00300086.
 XX 28-SEP-2001; 2001JP-00300086.
 XX (SRLS-) SRL KK.
 XX WPI; 2003-649087/62.
 DR N-PSDB; ABC56766.
 XX Measuring human thymidyllic-acid synthetase mRNA, by using primers that
 PT hybridize to full length cDNA of thymidyllic-acid synthetase gene but does
 PT not hybridize to variant cDNA in which specific exons of gene are
 PT deleted.
 XX Disclosure; Page 17-18; 28pp; Japanese.
 PS This invention relates to a novel method for measuring human thymidyllic
 CC acid synthetase (hts) mRNA (EC 2.1.1.45). Specifically, it comprises
 CC amplifying cDNA or mRNA of the hts gene using forward and reverse
 CC primers, where the forward primer does not hybridize to the variant cDNA
 CC in which exon 2 and exon 3 of the gene are deleted. Likewise the reverse
 CC primer does not hybridize to the variant cDNA in which exon 4 of the hts
 CC gene has been deleted. Accordingly, by measuring the amplified product of
 CC human thymidyllic acid synthetase it is possible to exactly measure only
 CC the active hts enzyme product, which is useful in the prognosis or
 CC treatment of cancer. Furthermore, the throughput of hts in a cancer cell
 CC can estimate the therapeutic effect of an anticancer agent. This
 CC polypeptide sequence is the human thymidyllic acid synthetase protein of
 CC the invention. NOTE: This protein is not further described in the
 CC specification but is given as an embedded protein in the sequence
 CC listing.
 XX Sequence 313 AA;
 SQ Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 26
 ADD22424
 ID ADD22424 standard; protein; 313 AA.
 XX ADD22424;
 XX 15-JAN-2004 (first entry)
 DT HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 74.
 DE tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
 KW colon; mouth; lung; prostatic; gynecological; human.
 KW Homo sapiens.
 OS JP2003111595-A.
 XX 15-APR-2003.
 PD 18-DEC-2003 (first entry)
 XX Human thymidyllic acid synthetase protein.
 DE human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.
 XX human; thymidyllic acid synthetase; hts; cancer; anticancer; EC 2.1.1.45.
 KW Homo sapiens.
 OS JP2003102480-A.
 XX 08-APR-2003.
 XX 28-SEP-2001; 2001JP-00300086.
 XX 28-SEP-2001; 2001JP-00300086.
 XX (SRLS-) SRL KK.
 XX WPI; 2003-649087/62.
 DR N-PSDB; ABC56766.
 XX Measuring human thymidyllic-acid synthetase mRNA, by using primers that
 PT hybridize to full length cDNA of thymidyllic-acid synthetase gene but does
 PT not hybridize to variant cDNA in which specific exons of gene are
 PT deleted.
 XX Disclosure; Page 17-18; 28pp; Japanese.
 PS This invention relates to a novel method for measuring human thymidyllic
 CC acid synthetase (hts) mRNA (EC 2.1.1.45). Specifically, it comprises
 CC amplifying cDNA or mRNA of the hts gene using forward and reverse
 CC primers, where the forward primer does not hybridize to the variant cDNA
 CC in which exon 2 and exon 3 of the gene are deleted. Likewise the reverse
 CC primer does not hybridize to the variant cDNA in which exon 4 of the hts
 CC gene has been deleted. Accordingly, by measuring the amplified product of
 CC human thymidyllic acid synthetase it is possible to exactly measure only
 CC the active hts enzyme product, which is useful in the prognosis or
 CC treatment of cancer. Furthermore, the throughput of hts in a cancer cell
 CC can estimate the therapeutic effect of an anticancer agent. This
 CC polypeptide sequence is the human thymidyllic acid synthetase protein of
 CC the invention. NOTE: This protein is not further described in the
 CC specification but is given as an embedded protein in the sequence
 CC listing.
 XX Sequence 313 AA;
 SQ Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 27
 ADE76649
 ID ADE76649 standard; protein; 313 AA.
 XX ADE76649;
 XX 29-JAN-2004 (first entry)
 DT Human thymidylate synthase mutant enzyme 24.
 DE thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW muten; 5-fluorouridine; 5-FdUR.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 103
 FT /note= "Wild-type Ser replaced by Thr"
 FT Misc-difference 204
 FT /note= "Wild-type Val replaced by Ala"
 FT

XX EP1316604-A1.
 PN
 XX
 PD
 XX
 XX 04-JUN-2003.
 XX
 PF 29-JUN-2002; 2002EP-00014489.
 XX
 PR 03-DEC-2001; 2001US-0334557P.
 XX
 XX (GEUR/) GEURTSSEN W.
 XX
 XX Loeb L, Geurtsen W;
 XX WPI; 2003-495241/47.
 DR
 XX
 XX
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 XX Claim 4; Page; 36pp; English.
 PS
 XX
 XX This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC the claims and the wild-type human TS sequence.
 XX
 XX Sequence 313 AA;
 SQ
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 28
 ADE76650
 ID ADE76650 standard; protein; 313 AA.
 XX
 XX ADE76650;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Human thymidylate synthase mutant enzyme 25.
 DE
 XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW muten; 5-fluorouridine; 5-FdUR.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 142 /note= "Wild-type Phe replaced by Ser"
 FT Misc-difference 225 /note= "Wild-type Phe replaced by Ile"
 FT
 XX EP1316604-A1.
 XX
 XX 04-JUN-2003.
 XX
 XX 29-JUN-2002; 2002EP-00014489.
 XX
 XX 03-DEC-2001; 2001US-0334557P.
 XX (GEUR/) GEURTSSEN W.
 XX
 XX Loeb L, Geurtsen W;
 XX WPI; 2003-495241/47.
 DR
 XX
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 XX Claim 4; Page; 36pp; English.
 PS
 XX This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC the claims and the wild-type human TS sequence.
 XX
 XX Sequence 313 AA;
 SQ
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 29
 ADE76628
 ID ADE76628 standard; protein; 313 AA.
 XX
 XX ADE76628;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Human thymidylate synthase mutant enzyme 3.
 DE
 XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW

KW mutein; 5-fluorouridine; 5-FdUR.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 84 /note= "Wild-type Val replaced by Ala"
 XX
 PN EPI316604-A1.
 XX
 PD 04-JUN-2003.
 XX
 PF 29-JUN-2002; 2002EP-00014489.
 XX
 PR 03-DEC-2001; 2001US-0334557P.
 XX
 PA (GEUR/) GEURTSSEN W.
 XX
 PI Loeb L, Geurtsen W;
 XX WPI; 2003-495241/47.
 DR
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 PS Claim 2; Page; 36pp; English.
 XX
 CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 30
 ADE76636
 ID ADE76636 standard; protein; 313 AA.
 XX
 AC ADE76636;
 XX
 XX 29-JAN-2004 (first entry)
 DT Human thymidylate synthase mutant enzyme 11.
 DE
 XX

KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW mutein; 5-fluorouridine; 5-FdUR.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 250 /note= "Wild-type His replaced by Leu"
 XX
 PN EPI316604-A1.
 XX
 PD 04-JUN-2003.
 XX
 PF 29-JUN-2002; 2002EP-00014489.
 XX
 PR 03-DEC-2001; 2001US-0334557P.
 XX
 PA (GEUR/) GEURTSSEN W.
 XX
 PI Loeb L, Geurtsen W;
 XX WPI; 2003-495241/47.
 DR
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 PS Claim 2; Page; 36pp; English.
 XX
 CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 Db 189 LMALPPCHAL 198
 RESULT 31
 ADE76643
 ID ADE76643 standard; protein; 313 AA.
 XX
 AC ADE76643;
 XX
 XX 29-JAN-2004 (first entry)
 DT

XX Human thymidylate synthase mutant enzyme 18.
DE thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
XX chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW muten; 5-fluorouridine; 5-FdUR.
XX Synthetic.
OS Homo sapiens.
XX
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 55 /note= "Wild-type Thr replaced by Ile"
FT Misc-difference 106 /note= "Wild-type Val replaced by Ala"
FT Misc-difference 284 /note= "Wild-type Lys replaced by Ile"
FT
XX EP1316604-A1.
PN
XX
XX
XX 04-JUN-2003.
XX
XX 29-JUN-2002; 2002EP-00014489.
XX
XX 03-DEC-2001; 2001US-0334557P.
XX (GEUR/) GEURTSSEN W.
XX
XX Loeb L, Geurtsen W;
XX WPI; 2003-495241/47.
XX
XX New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX
XX Claim 4; Page; 36pp; English.
XX
XX This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
CC result interfere with the DNA-metabolism of tumour cells. The protein
CC mutant is useful for the transfection of human cells which may be
CC affected by side effects due to chemotherapy with thymidylate synthase
CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
CC bone marrow cells. The protein mutant is also used for identifying new
CC nucleotide analogues that inhibit normal human thymidylate synthase, or for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198
|||||||

RESULT 32
ADE76626
ID ADE76626 standard; protein; 313 AA.
XX
XX ADE76626;
AC
XX 29-JAN-2004 (first entry)
DT
XX Human thymidylate synthase mutant enzyme 1.
DE
XX
XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW muten; 5-fluorouridine; 5-FdUR.
XX Synthetic.
OS Homo sapiens.
XX
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 23 /note= "Wild-type Glu replaced by Gly"
FT
XX EP1316604-A1.
PN
XX
XX 04-JUN-2003.
XX
XX 29-JUN-2002; 2002EP-00014489.
XX
XX 03-DEC-2001; 2001US-0334557P.
XX (GEUR/) GEURTSSEN W.
XX
XX Loeb L, Geurtsen W;
XX WPI; 2003-495241/47.
XX
XX New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX
XX Claim 2; Page; 36pp; English.
XX
XX This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
CC result interfere with the DNA-metabolism of tumour cells. The protein
CC mutant is useful for the transfection of human cells which may be
CC affected by side effects due to chemotherapy with thymidylate synthase
CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
CC bone marrow cells. The protein mutant is also used for identifying new
CC nucleotide analogues that inhibit normal human thymidylate synthase, for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
XX
SQ Sequence 313 AA;
Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMALPPCHAL 10
DB 189 LMALPPCHAL 198
|||||||

Db 189 LMALPPCHAL 198

RESULT 33

ADE76647

ID ADE76647 standard; protein; 313 AA.

XX AC ADE76647;

XX DT 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase mutant enzyme 22.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;

XX KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;

XX KW cytosstatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;

XX KW murein; 5-fluorouridine; 5-FdUR.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 6 /note= "Wild-type Ser replaced by Asn"

FT Misc-difference 69 /note= "Wild-type Asp replaced by Gln"

FT Misc-difference 211 /note= "Wild-type Gln replaced by Leu"

XX EP1316604-A1.

XX PD 04-JUN-2003.

XX PP 29-JUN-2002; 2002EP-00014489.

XX PR 03-DEC-2001; 2001US-0334557P.

XX PA (GEUR/) GEURTSSEN W.

XX PI Loeb L, Geurtsen W;

XX DR WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell

XX PT populations against toxicity from thymidylate synthase inhibitors,

XX PT differs from human wildtype thymidylate synthase in single, double or

XX PT multiple mutations.

XX PS Claim 4; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that

XX differs from human wild-type thymidylate synthase by one, two or more

XX mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a

XX result interfere with the DNA-metabolism of tumour cells. The protein

XX mutant is useful for the transfection of human cells which may be

XX affected by side effects due to chemotherapy with thymidylate synthase

XX inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,

XX or for transfection of early progenitor cells separated or grown from

XX nucleotide analogues that inhibit normal human thymidylate synthase, for

XX protecting human cell populations, preferably mucosa, against the toxic

XX manifestation of analogues that inhibit thymidylate synthase, or for

XX manufacturing cytostatic pharmaceutical and gene therapeutic compositions

XX for the protection of human mucosa against ulceration under chemotherapy

XX with thymidylate synthase inhibitors. A cDNA or a vector encoding the

XX mutant protein of the invention can also be used in gene therapy. The

XX present sequence is that of a mutant human thymidylate synthase (TS)

XX enzyme of the invention which displayed resistance to the TS-inhibitor

XX drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the

XX specification but was created by the indexer from information given in

XX the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;

Best Local Similarity 100.0%; Pred. No. 0.55;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

Db 189 LMALPPCHAL 198

RESULT 34

ADE76654

ID ADE76654 standard; protein; 313 AA.

XX AC ADE76654;

XX DT 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase mutant enzyme 29.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;

XX KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;

XX KW cytosstatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;

XX KW murein; 5-fluorouridine; 5-FdUR.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 38 /note= "Wild-type Gln replaced by His"

FT Misc-difference 104 /note= "Wild-type Lys replaced by Asp"

XX EP1316604-A1.

XX PD 04-JUN-2003.

XX PP 29-JUN-2002; 2002EP-00014489.

XX PR 03-DEC-2001; 2001US-0334557P.

XX PA (GEUR/) GEURTSSEN W.

XX PI Loeb L, Geurtsen W;

XX DR WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell

XX PT populations against toxicity from thymidylate synthase inhibitors,

XX PT differs from human wildtype thymidylate synthase in single, double or

XX PT multiple mutations.

XX PS Claim 4; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that

XX differs from human wild-type thymidylate synthase by one, two or more

XX mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a

XX result interfere with the DNA-metabolism of tumour cells. The protein

XX mutant is useful for the transfection of human cells which may be

XX affected by side effects due to chemotherapy with thymidylate synthase

XX inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,

XX or for transfection of early progenitor cells separated or grown from

XX bone marrow cells. The protein mutant is also used for identifying new

XX nucleotide analogues that inhibit normal human thymidylate synthase, for

XX protecting human cell populations, preferably mucosa, against the toxic

XX manifestation of analogues that inhibit thymidylate synthase, or for

XX manufacturing cytostatic pharmaceutical and gene therapeutic compositions

XX for the protection of human mucosa against ulceration under chemotherapy

XX with thymidylate synthase inhibitors. A cDNA or a vector encoding the

XX mutant protein of the invention can also be used in gene therapy. The

XX present sequence is that of a mutant human thymidylate synthase (TS)

XX enzyme of the invention which displayed resistance to the TS-inhibitor

XX drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the

XX specification but was created by the indexer from information given in

XX the claims and the wild-type human TS sequence.

CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 |||||
 Db 189 LMALPPCHAL 198

RESULT 35
 ADE76655
 ID ADE76655 standard; protein; 313 AA.

XX AC ADE76655;

XX DT 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase mutant enzyme 30.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW mutin; 5-fluorouridine; 5-FdUR.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 8 /note= "Wild-type Leu replaced by Gln"

FT Misc-difference 81 /note= "Wild-type Trp replaced by Gly"

FT Misc-difference 131 /note= "Wild-type Leu replaced by Val"

FT Misc-difference 230 /note= "Wild-type Tyr replaced by Phe"

FT EP1316604-A1.

XX 04-JUN-2003.

XX 29-JUN-2002; 2002EP-00014489.

XX 03-DEC-2001; 2001US-0334557P.

XX (GEUR/) GEURTSSEN W.

XX Loeb L, Geurtsen W;

XX WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell

XX populations against toxicity from thymidylate synthase inhibitors, or

XX multiple mutations.

XX Claim 4; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that

XX differs from human wild-type thymidylate synthase by one, two or more

XX mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a

XX result interfere with the DNA-metabolism of tumour cells. The protein

XX mutant is useful for the transfection of human cells which may be

XX affected by side effects due to chemotherapy with thymidylate synthase

XX inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,

XX or for transfection of early progenitor cells separated or grown from

XX bone marrow cells. The protein mutant is also used for identifying new

CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10

|||||

Db 189 LMALPPCHAL 198

RESULT 36

ADE76648

ID ADE76648 standard; protein; 313 AA.

XX AC ADE76648;

XX DT 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase mutant enzyme 23.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;

XX chemotherapy; thymidylate synthase inhibitor; early progenitor cell;

XX cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;

XX mutin; 5-fluorouridine; 5-FdUR.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 5 /note= "Wild-type Gly replaced by Asp"

FT Misc-difference 13 /note= "Wild-type Leu replaced by Arg"

FT Misc-difference 231 /note= "Wild-type Ala replaced by Thr"

FT EP1316604-A1.

XX 04-JUN-2003.

XX 29-JUN-2002; 2002EP-00014489.

XX 03-DEC-2001; 2001US-0334557P.

XX (GEUR/) GEURTSSEN W.

XX Loeb L, Geurtsen W;

XX WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell

XX populations against toxicity from thymidylate synthase inhibitors, or

XX multiple mutations.

XX Claim 4; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that

XX differs from human wild-type thymidylate synthase by one, two or more

CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.

XX
 XX Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 |||||
 DB 189 LMALPPCHAL 198

RESULT 37
 ADE76651
 ID ADE76651 standard; protein; 313 AA.

AC ADE76651;

XX 29-JAN-2004 (first entry)

XX Human thymidylate synthase mutant enzyme 26.

XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW mutin; 5-fluorouridine; 5-FdUR.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 17 /note= "Wild-type Ala replaced by Thr"

FT Misc-difference 116 /note= "Wild-type Asp replaced by Ala"

FT Misc-difference 254 /note= "Wild-type Asp replaced by Glu"

XX EP1316604-A1.

XX 04-JUN-2003.

XX 29-JUN-2002; 2002EP-00014489.

XX 03-DEC-2001; 2001US-0334557P.

XX (GEUR/) GEURTSSEN W.

XX Loeb L, Geurtsen W;

XX WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,

PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.

XX Claim 4; Page; 36pp; English.

XX This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.

XX Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
 |||||
 DB 189 LMALPPCHAL 198

RESULT 38

ADE76637

ID ADE76637 standard; protein; 313 AA.

XX AC ADE76637;

XX 29-JAN-2004 (first entry)

XX Human thymidylate synthase mutant enzyme 12.

XX thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW mutin; 5-fluorouridine; 5-FdUR.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 254 /note= "Wild-type Asp replaced by Glu"

XX EP1316604-A1.

XX 04-JUN-2003.

XX 29-JUN-2002; 2002EP-00014489.

XX 03-DEC-2001; 2001US-0334557P.

XX (GEUR/) GEURTSSEN W.

XX Loeb L, Geurtsen W;

XX WPI; 2003-495241/47.

XX New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX Claim 2; Page; 36pp; English.
XX This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
CC result interfere with the DNA-metabolism of tumour cells. The protein
CC mutant is useful for the transfection of human cells which may be
CC affected by side effects due to chemotherapy with thymidylate synthase
CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
CC bone marrow cells. The protein mutant is also used for identifying new
CC nucleotide analogues that inhibit normal human thymidylate synthase, for
CC protecting human cell populations, preferably mucosa, against the toxic
CC manifestation of analogues that inhibit thymidylate synthase, or for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
XX Sequence 313 AA;
SQ Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198
RESULT 39
ADE76631
ID ADE76631 standard; protein; 313 AA.
AC ADE76631;
XX 29-JAN-2004 (first entry)
DT Human thymidylate synthase mutant enzyme 6.
DE thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW muten; 5-fluorouridine; 5-FdUR.
XX Synthetic.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 116
FT /note= "Wild-type Asp replaced by Ala"
XX EP1316604-Al.
PN 04-JUN-2003.
XX 29-JUN-2002; 2002EP-00014489.
XX 03-DEC-2001; 2001US-0334557P.
XX (GEUR/) GEURTSSEN W.
XX

PI Loeb L, Geurtsen W;
XX WPI; 2003-495241/47.
XX New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX Claim 2; Page; 36pp; English.
XX This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
CC result interfere with the DNA-metabolism of tumour cells. The protein
CC mutant is useful for the transfection of human cells which may be
CC affected by side effects due to chemotherapy with thymidylate synthase
CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
CC bone marrow cells. The protein mutant is also used for identifying new
CC nucleotide analogues that inhibit normal human thymidylate synthase, for
CC protecting human cell populations, preferably mucosa, against the toxic
CC manifestation of analogues that inhibit thymidylate synthase, or for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
XX Sequence 313 AA;
SQ Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198
RESULT 40
ADE76627
ID ADE76627 standard; protein; 313 AA.
XX ADE76627;
AC ADE76627;
XX 29-JAN-2004 (first entry)
DT Human thymidylate synthase mutant enzyme 2.
DE thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW muten; 5-fluorouridine; 5-FdUR.
XX Synthetic.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 53
FT /note= "Wild-type Thr replaced by Ser"
XX EP1316604-Al.
PN 04-JUN-2003.
XX 29-JUN-2002; 2002EP-00014489.
XX 03-DEC-2001; 2001US-0334557P.
XX (GEUR/) GEURTSSEN W.
XX

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XX PA (GEUR/) GEURTSSEN W.
XX PR Loeb L, Geurtsen W;
XX PI WPI; 2003-495241/47.
XX DR New thymidylate synthase mutant, useful for protecting normal cell
XX PT populations against toxicity from thymidylate synthase inhibitors,
XX PT differs from human wildtype thymidylate synthase in single, double or
XX PT multiple mutations.
XX PS Claim 2; Page; 36pp; English.
XX CC This invention relates to a novel thymidylate synthase mutant that
XX CC differs from human wild-type thymidylate synthase by one, two or more
XX CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
XX CC result interfere with the DNA-metabolism of tumour cells. The protein
XX CC mutant is useful for the transfection of human cells which may be
XX CC affected by side effects due to chemotherapy with thymidylate synthase
XX CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
XX CC or for transfection of early progenitor cells separated or grown from
XX CC nucleotide analogues that inhibit normal human thymidylate synthase, for
XX CC protecting human cell populations, preferably mucosa, against the toxic
XX CC manifestation of cytostatic pharmaceutical and gene therapeutic compositions
XX CC for the protection of human mucosa against ulceration under chemotherapy
XX CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
XX CC mutant protein of the invention can also be used in gene therapy. The
XX CC present sequence is that of a mutant human thymidylate synthase (TS)
XX CC enzyme of the invention which displayed resistance to the TS-inhibitor
XX CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
XX CC specification but was created by the indexer from information given in
XX CC the claims and the wild-type human TS sequence.
XX SQ Sequence 313 AA;
    Query Match 100.0%; Score 56; DB 7; Length 313;
    Best Local Similarity 100.0%; Pred. No. 0.55;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198
RESULT 41
ADE76630
AC ADE76630 standard; protein; 313 AA.
XX AC ADE76630;
XX DT 29-JAN-2004 (first entry)
XX DE Human thymidylate synthase mutant enzyme 5.
XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
XX KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
XX KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
XX KW muten; 5-fluorouridine; 5-FdUR.
XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT Misc-difference 110 /note= "Wild-type Asp replaced by Glu"
XX FT EP1316604-A1.
XX PN 04-JUN-2003.
XX PD
XX

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PF 29-JUN-2002; 2002EP-00014489.
XX 03-DEC-2001; 2001US-0334557P.
XX PR (GEUR/) GEURTSSEN W.
XX PA Loeb L, Geurtsen W;
XX PI WPI; 2003-495241/47.
XX DR New thymidylate synthase mutant, useful for protecting normal cell
XX PT populations against toxicity from thymidylate synthase inhibitors,
XX PT differs from human wildtype thymidylate synthase in single, double or
XX PT multiple mutations.
XX PS Claim 2; Page; 36pp; English.
XX CC This invention relates to a novel thymidylate synthase mutant that
XX CC differs from human wild-type thymidylate synthase by one, two or more
XX CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
XX CC result interfere with the DNA-metabolism of tumour cells. The protein
XX CC mutant is useful for the transfection of human cells which may be
XX CC affected by side effects due to chemotherapy with thymidylate synthase
XX CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
XX CC or for transfection of early progenitor cells separated or grown from
XX CC nucleotide analogues that inhibit normal human thymidylate synthase, for
XX CC protecting human cell populations, preferably mucosa, against the toxic
XX CC manifestation of cytostatic pharmaceutical and gene therapeutic compositions
XX CC for the protection of human mucosa against ulceration under chemotherapy
XX CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
XX CC mutant protein of the invention can also be used in gene therapy. The
XX CC present sequence is that of a mutant human thymidylate synthase (TS)
XX CC enzyme of the invention which displayed resistance to the TS-inhibitor
XX CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
XX CC specification but was created by the indexer from information given in
XX CC the claims and the wild-type human TS sequence.
XX SQ Sequence 313 AA;
    Query Match 100.0%; Score 56; DB 7; Length 313;
    Best Local Similarity 100.0%; Pred. No. 0.55;
    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198
RESULT 42
ADE76639
ID ADE76639 standard; protein; 313 AA.
XX AC ADE76639;
XX DT 29-JAN-2004 (first entry)
XX DE Human thymidylate synthase mutant enzyme 14.
XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
XX KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
XX KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
XX KW muten; 5-fluorouridine; 5-FdUR.
XX OS Synthetic.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT Misc-difference 254 /note= "Wild-type Asp replaced by Asn"
XX FT EP1316604-A1.
XX PN
XX

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XX PD 04-JUN-2003.
 XX FT
 XX PP 29-JUN-2002; 2002EP-00014489.
 XX PR 03-DEC-2001; 2001US-0334557P.
 XX PA (GEUR/) GEURTSSEN W.
 XX PI Loeb L, Geurtsen W;
 XX PD WPI; 2003-495241/47.
 XX PP
 XX PT New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX PS
 XX PS Claim 2; Page; 36pp; English.
 XX CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 1 LMALPPCHAL 10
 |||||
 Db 189 LMALPPCHAL 198
 RESULT 43
 ADE76652
 ID ADE76652 standard; protein; 313 AA.
 XX AC ADE76652;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human thymidylate synthase mutant enzyme 27.
 XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW muten; 5-fluorouridine; 5-FdUR.
 XX OS Synthetic.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 117

FT Misc-difference 169 /note= "Wild-type Phe replaced by Ser"
 FT /note= "Wild-type Lys replaced by Arg"
 FT Misc-difference 254 /note= "Wild-type Asp replaced by Glu"
 XX PN EP1316604-A1.
 XX PD 04-JUN-2003.
 XX PP 29-JUN-2002; 2002EP-00014489.
 XX PR 03-DEC-2001; 2001US-0334557P.
 XX PA (GEUR/) GEURTSSEN W.
 XX PI Loeb L, Geurtsen W;
 XX PD WPI; 2003-495241/47.
 XX PP
 XX PT New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX PS
 XX PS Claim 4; Page; 36pp; English.
 XX CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;
 QY 1 LMALPPCHAL 10
 |||||
 Db 189 LMALPPCHAL 198
 RESULT 44
 ADE76641
 ID ADE76641 standard; protein; 313 AA.
 XX AC ADE76641;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human thymidylate synthase mutant enzyme 16.
 XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW

KW mutein; 5-fluorouridine; 5-FdUR.
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 258 /note= "Wild-type Tyr replaced by Phe"
 XX
 XX
 PN EPI316604-A1.
 XX
 XX
 PD 04-JUN-2003.
 XX
 XX
 PF 29-JUN-2002; 2002EP-00014489.
 XX
 PR 03-DEC-2001; 2001US-0334557P.
 XX
 XX (GEUR/) GEURTSSEN W.
 PA
 FI Loeb L, Geurtsen W;
 XX
 XX WPI; 2003-495241/47.
 DR
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 XX Claim 2; Page; 36pp; English.
 PS
 XX This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 189 LMALPPCHAL 198
 RESULT 45
 ADE76644
 ID ADE76644 standard; protein; 313 AA.
 XX ADE76644;
 AC
 XX
 XX 29-JAN-2004 (first entry)
 DT Human thymidylate synthase mutant enzyme 19.
 DE
 XX

KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW mutein; 5-fluorouridine; 5-FdUR.
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 5 /note= "Wild-type Gly replaced by Ser"
 FT
 FT Misc-difference 78 /note= "Wild-type Arg replaced by Cys"
 FT
 FT Misc-difference 219 /note= "Wild-type Met replaced by Ile"
 FT
 XX
 PN EPI316604-A1.
 XX
 XX
 PD 04-JUN-2003.
 XX
 XX
 PF 29-JUN-2002; 2002EP-00014489.
 XX
 PR 03-DEC-2001; 2001US-0334557P.
 XX
 XX (GEUR/) GEURTSSEN W.
 PA
 FI Loeb L, Geurtsen W;
 XX
 XX WPI; 2003-495241/47.
 DR
 XX New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors, or
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.
 XX
 XX Claim 4; Page; 36pp; English.
 PS
 XX This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of a mutant human thymidylate synthase (TS)
 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
 CC specification but was created by the indexer from information given in
 CC the claims and the wild-type human TS sequence.
 XX
 SQ Sequence 313 AA;
 Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMALPPCHAL 10
 DB 189 LMALPPCHAL 198
 RESULT 46
 ADE76656
 ID ADE76656 standard; protein; 313 AA.

XX
AC ADE76656;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human thymidylate synthase mutant enzyme 31.
XX
KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW mutin; 5-fluorouridine; 5-FdUR.
XX
OS Synthetic.
OS Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 51 /note= "Wild-type Thr replaced by Ser"
FT Misc-difference 82 /note= "Wild-type Lys replaced by Gln"
FT Misc-difference 99 /note= "Wild-type Lys replaced by Asp"
FT Misc-difference 171 /note= "Wild-type Asn replaced by Ser"
XX
PN EP1316604-A1.
XX
PD 04-JUN-2003.
XX
PF 29-JUN-2002; 2002EP-00014489.
XX
PR 03-DEC-2001; 2001US-0334557P.
XX
PA (GEUR/) GEURTSSEN W.
XX
PI Loeb L, Geurtsen W;
XX
DR WPI; 2003-495241/47.
XX
PT New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX
PS Claim 4; Page; 36pp; English.
XX
CC This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
CC result interfere with the DNA-metabolism of tumour cells. The protein
CC mutant is useful for the transfection of human cells which may be
CC affected by side effects due to chemotherapy with thymidylate synthase
CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
CC bone marrow cells. The protein mutant is also used for identifying new
CC nucleotide analogues that inhibit normal human thymidylate synthase, for
CC protecting human cell populations, preferably mucosa, against the toxic
CC manifestation of analogues that inhibit thymidylate synthase, or for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
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SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 189 LMALPPCHAL 198
RESULT 47
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ID ADE76634 standard; protein; 313 AA.
XX
AC ADE76634;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human thymidylate synthase mutant enzyme 9.
XX
KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW mutin; 5-fluorouridine; 5-FdUR.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild-type Ser replaced by Gly"
XX
PN EP1316604-A1.
XX
PD 04-JUN-2003.
XX
PF 29-JUN-2002; 2002EP-00014489.
XX
PR 03-DEC-2001; 2001US-0334557P.
XX
PA (GEUR/) GEURTSSEN W.
XX
PI Loeb L, Geurtsen W;
XX
DR WPI; 2003-495241/47.
XX
PT New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX
PS Claim 2; Page; 36pp; English.
XX

This invention relates to a novel thymidylate synthase mutant that differs from human wild-type thymidylate synthase by one, two or more mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a result interfere with the DNA-metabolism of tumour cells. The protein mutant is useful for the transfection of human cells which may be affected by side effects due to chemotherapy with thymidylate synthase inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells, or for transfection of early progenitor cells separated or grown from bone marrow cells. The protein mutant is also used for identifying new nucleotide analogues that inhibit normal human thymidylate synthase, for protecting human cell populations, preferably mucosa, against the toxic manifestation of analogues that inhibit thymidylate synthase, or for manufacturing cytostatic pharmaceutical and gene therapeutic compositions for the protection of human mucosa against ulceration under chemotherapy with thymidylate synthase inhibitors. A cDNA or a vector encoding the mutant protein of the invention can also be used in gene therapy. The present sequence is that of a mutant human thymidylate synthase (TS) enzyme of the invention which displayed resistance to the TS-inhibitor drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the specification but was created by the indexer from information given in the claims and the wild-type human TS sequence.
XX
SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
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 DB 189 LMALPPCHAL 198

RESULT 48
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 ID ADE76625 standard; protein; 313 AA.

XX AC ADE76625;

XX 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase wild-type sequence.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme.

XX OS Homo sapiens.

XX FN EP1316604-A1.

XX PD 04-JUN-2003.

XX PF 29-JUN-2002; 2002EP-00014489.

XX PR 03-DEC-2001; 2001US-0334557P.

XX PA (GEUR/) GEURTSSEN W.

XX PI Loeb L, Geurtsen W;

XX DR WPI; 2003-495241/47.

XX PT New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.

XX PS Disclosure; Fig 2; 36pp; English.

XX CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
 CC mutant is useful for the transfection of human cells which may be
 CC affected by side effects due to chemotherapy with thymidylate synthase
 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
 CC protecting human cell populations, preferably mucosa, against the toxic
 CC manifestation of analogues that inhibit thymidylate synthase, or for
 CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
 CC present sequence is that of the wild-type human thymidylate synthase (TS)
 CC enzyme from which the mutants of the invention were created.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
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DB 189 LMALPPCHAL 198

RESULT 49

ID ADE76629 standard; protein; 313 AA.

XX AC ADE76629;

XX DT 29-JAN-2004 (first entry)

XX DE Human thymidylate synthase mutant enzyme 4.

XX KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
 KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
 KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
 KW muten; 5-fluorouridine; 5-FdUR.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 93

XX FT /note= "Wild-type Lys replaced by Glu"

XX FN EP1316604-A1.

XX PD 04-JUN-2003.

XX PF 29-JUN-2002; 2002EP-00014489.

XX PR 03-DEC-2001; 2001US-0334557P.

XX PA (GEUR/) GEURTSSEN W.

XX PI Loeb L, Geurtsen W;

XX DR WPI; 2003-495241/47.

XX PT New thymidylate synthase mutant, useful for protecting normal cell
 PT populations against toxicity from thymidylate synthase inhibitors,
 PT differs from human wildtype thymidylate synthase in single, double or
 PT multiple mutations.

XX PS Claim 2; Page; 36pp; English.

XX CC This invention relates to a novel thymidylate synthase mutant that
 CC differs from human wild-type thymidylate synthase by one, two or more
 CC mutations. Various chemotherapeutic drugs inhibit the TS enzyme and as a
 CC result interfere with the DNA-metabolism of tumour cells. The protein
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 CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
 CC or for transfection of early progenitor cells separated or grown from
 CC bone marrow cells. The protein mutant is also used for identifying new
 CC nucleotide analogues that inhibit normal human thymidylate synthase, for
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 CC manifestation of analogues that inhibit thymidylate synthase, or for
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 CC for the protection of human mucosa against ulceration under chemotherapy
 CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
 CC mutant protein of the invention can also be used in gene therapy. The
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 CC enzyme of the invention which displayed resistance to the TS-inhibitor
 CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
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 CC the claims and the wild-type human TS sequence.

XX SQ Sequence 313 AA;

Query Match 100.0%; Score 56; DB 7; Length 313;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 56; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
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DB 189 LMALPPCHAL 198

Search completed: February 17, 2006, 02:40:16
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DB 189 LMALPPCHAL 198

RESULT 50
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ID ADE76638 standard; protein; 313 AA.
AC ADE76638;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human thymidylate synthase mutant enzyme 13.
XX
KW thymidylate synthase; chemotherapeutic drug; DNA-metabolism; tumour cell;
KW chemotherapy; thymidylate synthase inhibitor; early progenitor cell;
KW cytostatic; human mucosa ulceration; gene therapy; human; enzyme; mutant;
KW mutetin; 5-fluorouridine; 5-FdUR.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 254
FT /note= "Wild-type Asp replaced by Ala"
XX
PN EP1316604-Al.
XX
PD 04-JUN-2003.
XX
XX 29-JUN-2002; 2002EP-00014489.
XX
PR 03-DEC-2001; 2001US-0334557P.
XX
PA (GEUR/) GEURTSSEN W.
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PI Loeb L, Geurtsen W;
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WPI; 2003-495241/47.
XX
XX New thymidylate synthase mutant, useful for protecting normal cell
PT populations against toxicity from thymidylate synthase inhibitors,
PT differs from human wildtype thymidylate synthase in single, double or
PT multiple mutations.
XX
PS Claim 2; Page; 36pp; English.
XX
CC This invention relates to a novel thymidylate synthase mutant that
CC differs from human wild-type thymidylate synthase by one, two or more
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CC mutant is useful for the transfection of human cells which may be
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CC inhibitors, for the ex-vivo or in vivo transfection of bone marrow cells,
CC or for transfection of early progenitor cells separated or grown from
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CC nucleotide analogues that inhibit normal human thymidylate synthase, for
CC protecting human cell populations, preferably mucosa, against the toxic
CC manifestation of analogues that inhibit thymidylate synthase, or for
CC manufacturing cytostatic pharmaceutical and gene therapeutic compositions
CC for the protection of human mucosa against ulceration under chemotherapy
CC with thymidylate synthase inhibitors. A cDNA or a vector encoding the
CC mutant protein of the invention can also be used in gene therapy. The
CC present sequence is that of a mutant human thymidylate synthase (TS)
CC enzyme of the invention which displayed resistance to the TS-inhibitor
CC drug 5-fluorouridine (5-FdUR). Note: This sequence does not appear in the
CC specification but was created by the indexer from information given in
CC the claims and the wild-type human TS sequence.
XX
SQ Sequence 313 AA;

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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:45:36 ; Search time 17 Seconds
(without alignments)
8.362 Million cell updates/sec

Title: US-10-734-049B-188
Perfect score: 56
Sequence: 1 LMAPPECHAL 10

Scoring table: BLOSUM62
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Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	47	83.9	225	7	US-11-055-822-990
3	40	71.4	264	7	US-11-165-067A-28
4	40	71.4	264	7	US-11-165-067A-45
5	36	64.3	111	7	US-11-184-005-5
6	35	62.5	232	6	US-10-821-234-1023
7	34	60.7	111	7	US-11-072-512-2358
8	33	58.9	23	7	US-11-068-783-112
9	33	58.9	271	6	US-10-353-783-52
10	33	58.9	296	7	US-11-169-041-233
11	33	58.9	688	7	US-11-131-035-2
12	33	58.9	1042	7	US-11-067-811-1
13	33	58.9	1047	7	US-11-124-367A-388
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					Sequence 52, Appl
					Sequence 233, Ap
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					Sequence 388, Ap
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					Sequence 387, Ap
					Sequence 2662, Ap
					Sequence 2271, Ap
					Sequence 824, Ap
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					Sequence 5, Appl
					Sequence 45, Appl
					Sequence 34, Appl
					Sequence 892, Ap
					Sequence 893, Ap
					Sequence 158, Ap

Sequence 3, Appl	6	US-10-880-764-3	413	57.1	32
Sequence 110, App	6	US-10-986-501-110	457	57.1	32
Sequence 3794, Ap	7	US-11-072-512-3794	482	57.1	32
Sequence 201, App	6	US-10-667-295-201	486	57.1	32
Sequence 2580, Ap	7	US-11-072-512-2580	510	57.1	32
Sequence 2, Appl	6	US-10-972-053-2	782	57.1	32
Sequence 8, Appl	6	US-10-972-053-8	782	57.1	32
Sequence 10, Appl	6	US-10-972-053-10	784	57.1	32
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Sequence 70, Appl	1137	US-11-012-762-70	1137	57.1	32
Sequence 336, App	7	US-11-198-847-336	15	55.4	31
Sequence 337, App	7	US-11-198-847-337	15	55.4	31
Sequence 334, App	7	US-11-198-847-334	17	55.4	31
Sequence 335, App	7	US-11-198-847-335	17	55.4	31
Sequence 235, App	7	US-11-198-847-235	19	55.4	31
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Sequence 92, Appl	7	US-11-120-308-92	60	55.4	31
Sequence 14, Appl	7	US-11-198-847-14	72	55.4	31
Sequence 221, App	7	US-11-198-847-221	72	55.4	31
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Sequence 3756, Ap	7	US-11-072-512-3756	221	55.4	31
Sequence 2017, Ap	7	US-11-072-512-2017	263	55.4	31
Sequence 196, App	6	US-10-714-887-196	286	55.4	31
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Sequence 24, Appl	7	US-11-077-386-24	346	55.4	31
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Sequence 64, Appl	7	US-11-031-206-64	436	55.4	31
Sequence 10575, A	7	US-11-098-686-10575	446	55.4	31
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Sequence 879, App	6	US-10-821-234-879	670	55.4	31
Sequence 426, App	6	US-10-131-826A-426	747	55.4	31
Sequence 10, Appl	7	US-11-065-695-10	1184	55.4	31
Sequence 6, Appl	7	US-11-004-057-6	1302	55.4	31
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Sequence 32, Appl	6	US-10-453-372-32	3546	55.4	31
Sequence 116, Ap	7	US-11-108-172-116	5405	55.4	31
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Sequence 2746, Ap	7	US-11-072-512-2746	105	53.6	30
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Sequence 10969, A	7	US-11-098-686-10969	149	53.6	30
Sequence 2601, Ap	6	US-11-072-512-2601	224	53.6	30
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Sequence 76, Appl	6	US-10-454-437-76	278	53.6	30
Sequence 2, Appl	7	US-11-067-121-2	295	53.6	30
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Sequence 342, App	7	US-11-156-084-342	306	53.6	30
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Sequence 3018, Ap	7	US-11-072-512-3018	766	53.6	30

99 30 53.6 2644 6 US-10-770-726-45 Sequence 45, Appl
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101 30 53.6 3095 7 US-11-235-732-4 Sequence 4, Appl
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104 29 51.8 11 7 US-11-193-197-10 Sequence 10, Appl
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106 29 51.8 12 6 US-10-511-722-3 Sequence 3, Appl
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108 29 51.8 41 6 US-10-511-722-2 Sequence 2, Appl
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111 29 51.8 86 6 US-10-511-722-1 Sequence 1, Appl
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118 29 51.8 136 7 US-11-072-512-3447 Sequence 3447, Ap
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121 29 51.8 180 6 US-10-453-372-164 Sequence 164, App
122 29 51.8 200 6 US-10-793-626-394 Sequence 394, App
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127 29 51.8 253 7 US-11-015-546A-2 Sequence 2, Appl
128 29 51.8 267 6 US-10-883-512-89 Sequence 89, Appl
129 29 51.8 269 7 US-11-015-546A-10 Sequence 10, Appl
130 29 51.8 274 7 US-11-015-546A-12 Sequence 12, Appl
131 29 51.8 274 7 US-11-143-980-58 Sequence 58, Appl
132 29 51.8 306 7 US-11-017-550-45 Sequence 45, Appl
133 29 51.8 306 7 US-11-137-850-6 Sequence 6, Appl
134 29 51.8 317 7 US-11-090-617-702 Sequence 702, App
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136 29 51.8 369 7 US-11-105-268-60 Sequence 60, Appl
137 29 51.8 381 6 US-10-453-372-128 Sequence 128, App
138 29 51.8 444 7 US-11-053-554A-67 Sequence 67, Appl
139 29 51.8 481 7 US-11-072-512-2394 Sequence 2394, Ap
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143 29 51.8 538 6 US-10-717-580-33 Sequence 33, Appl
144 29 51.8 540 6 US-10-821-234-1395 Sequence 1395, Ap
145 29 51.8 560 6 US-10-763-712A-79 Sequence 79, Appl
146 29 51.8 568 7 US-11-098-686-10558 Sequence 10558, A
147 29 51.8 580 6 US-10-453-372-138 Sequence 138, App
148 29 51.8 580 6 US-10-453-372-144 Sequence 144, App
149 29 51.8 585 7 US-11-127-877-63 Sequence 63, Appl
150 29 51.8 638 7 US-11-072-512-2626 Sequence 2626, Ap
151 29 51.8 761 6 US-10-453-372-126 Sequence 126, App
152 29 51.8 823 6 US-10-453-372-122 Sequence 122, App
153 29 51.8 823 6 US-10-453-372-124 Sequence 124, App
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155 29 51.8 826 6 US-10-453-372-156 Sequence 156, App
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157 29 51.8 826 6 US-10-453-372-172 Sequence 172, App
158 29 51.8 826 6 US-10-453-372-174 Sequence 174, App
159 29 51.8 826 6 US-10-453-372-176 Sequence 176, App
160 29 51.8 832 6 US-10-453-372-120 Sequence 120, App
161 29 51.8 837 7 US-11-127-877-74 Sequence 74, Appl
162 29 51.8 1062 6 US-10-821-234-1079 Sequence 1079, Ap
163 29 51.8 1085 7 US-10-523-477-13 Sequence 13, Appl
164 29 51.8 1087 6 US-11-117-169-10 Sequence 10, Appl
165 29 51.8 1115 6 US-10-922-2328-60 Sequence 60, Appl
166 29 51.8 1481 7 US-11-077-386-30 Sequence 30, Appl
167 29 51.8 1733 7 US-11-182-016-21 Sequence 21, Appl
168 29 51.8 1798 6 US-10-995-561-1033 Sequence 1033, Ap
169 29 51.8 1798 6 US-10-995-561-1034 Sequence 1034, Ap
170 29 51.8 1798 7 US-11-080-991-96 Sequence 96, Appl
171 29 51.8 1960 7 US-11-077-386-29 Sequence 29, Appl

7 51.8 2061 7 US-11-077-386-27 Sequence 27, Appl
7 2061 7 US-11-169-041-179 Sequence 179, App
6 2333 6 US-10-453-372-170 Sequence 170, App
29 51.8 2662 6 US-10-453-372-114 Sequence 114, App
29 51.8 2724 6 US-10-453-372-148 Sequence 148, App
29 51.8 2733 6 US-10-453-372-136 Sequence 136, App
29 51.8 2733 6 US-10-453-372-142 Sequence 142, App
6 2733 6 US-10-453-372-146 Sequence 146, App
29 51.8 2733 6 US-10-453-372-150 Sequence 150, App
29 51.8 2733 6 US-10-453-372-154 Sequence 154, App
29 51.8 2759 6 US-10-453-372-168 Sequence 168, App
29 51.8 2765 6 US-10-453-372-116 Sequence 116, App
6 6738 6 US-10-922-232B-56 Sequence 56, Appl
16 7 US-11-052-168A-30 Sequence 30, Appl
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28 50.0 55 6 US-10-467-657-2084 Sequence 2084, Ap
28 50.0 55 6 US-10-511-538-233 Sequence 233, App
28 50.0 105 6 US-10-793-626-554 Sequence 554, App
28 50.0 108 6 US-11-034-281-52 Sequence 52, Appl
28 50.0 114 7 US-11-072-512-2295 Sequence 2295, Ap
28 50.0 123 7 US-10-821-234-1156 Sequence 1156, Ap
28 50.0 124 6 US-10-118-590-38 Sequence 38, Appl
28 50.0 126 6 US-10-518-955-2 Sequence 2, Appl
28 50.0 131 5 US-09-978-360A-415 Sequence 415, App
28 50.0 133 7 US-11-072-512-3128 Sequence 3128, Ap
28 50.0 133 7 US-11-072-512-2149 Sequence 2149, Ap
28 50.0 169 6 US-10-867-168-1 Sequence 1, Appl
28 50.0 185 6 US-10-967-527A-10 Sequence 10, Appl
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28 50.0 190 5 US-09-978-360A-594 Sequence 594, App
28 50.0 224 6 US-10-467-657-5378 Sequence 5378, Ap
28 50.0 246 7 US-11-072-512-2232 Sequence 2232, Ap
28 50.0 246 7 US-11-072-512-2243 Sequence 2243, Ap
28 50.0 250 6 US-10-821-234-987 Sequence 987, App
28 50.0 262 7 US-11-074-176-8 Sequence 8, Appl
28 50.0 262 7 US-10-467-657-2200 Sequence 2200, Ap
28 50.0 276 6 US-10-131-826A-242 Sequence 242, App
28 50.0 322 6 US-10-467-657-166 Sequence 166, App
28 50.0 322 6 US-10-467-657-3062 Sequence 3062, Ap
28 50.0 337 7 US-11-008-570-126 Sequence 126, App
28 50.0 372 6 US-10-650-326B-13 Sequence 13, Appl
28 50.0 372 6 US-11-246-555-33 Sequence 33, Appl
28 50.0 372 7 US-11-148-280-2 Sequence 2, Appl
28 50.0 372 7 US-11-148-280-3 Sequence 3, Appl
28 50.0 376 7 US-11-213-368-6 Sequence 6, Appl
28 50.0 376 7 US-11-213-368-14 Sequence 14, Appl
28 50.0 391 6 US-10-793-626-2348 Sequence 2348, Ap
28 50.0 406 6 US-10-467-657-5504 Sequence 5504, Ap
28 50.0 434 7 US-11-241-956-5 Sequence 5, Appl
28 50.0 483 7 US-11-184-574-4 Sequence 4, Appl
5 554 5 US-09-978-360A-410 Sequence 410, App
28 50.0 555 7 US-11-024-959-370 Sequence 270, App
28 50.0 565 6 US-10-485-517-300 Sequence 300, App
28 50.0 587 7 US-11-024-959-412 Sequence 412, App
28 50.0 742 7 US-11-191-374-46 Sequence 46, Appl
28 50.0 742 7 US-11-191-375-46 Sequence 46, Appl
28 50.0 742 7 US-11-191-588-46 Sequence 46, Appl
28 50.0 775 7 US-11-072-175-180 Sequence 180, App
28 50.0 788 6 US-10-505-263-85 Sequence 85, Appl
28 50.0 791 6 US-10-972-053-4 Sequence 4, Appl
28 50.0 794 7 US-10-218-986-2 Sequence 2, Appl
28 50.0 820 6 US-10-821-234-1176 Sequence 1176, Ap
28 50.0 1041 6 US-10-995-561-780 Sequence 780, App
28 50.0 1041 6 US-10-995-561-782 Sequence 782, App
28 50.0 1097 6 US-10-995-561-781 Sequence 781, App
28 50.0 1113 7 US-11-067-811-4 Sequence 4, Appl
28 50.0 1138 7 US-11-012-762-28 Sequence 28, Appl
28 50.0 1138 7 US-11-049-536-21 Sequence 21, Appl
28 50.0 1192 7 US-11-149-003-18 Sequence 18, Appl
28 50.0 1207 7 US-11-149-003-20 Sequence 20, Appl
28 50.0 1251 7 US-11-149-003-16 Sequence 16, Appl

245	28	50.0	1342	7	US-11-149-003-24	Sequence 24, Appl	318	27	48.2	375	6	US-10-995-561-540	Sequence 540, App
246	28	50.0	1477	7	US-11-149-003-8	Sequence 8, Appl	319	27	48.2	375	6	US-10-987-856-17	Sequence 17, Appl
247	28	50.0	1512	7	US-11-149-003-10	Sequence 10, Appl	320	27	48.2	391	6	US-10-770-726-59	Sequence 59, Appl
248	28	50.0	1535	6	US-11-149-003-14	Sequence 14, Appl	321	27	48.2	400	7	US-11-186-284-155	Sequence 155, App
249	28	50.0	1558	6	US-10-329-258-14	Sequence 14, Appl	322	27	48.2	411	6	US-10-989-649-3	Sequence 3, Appl
250	28	50.0	1570	7	US-11-149-003-12	Sequence 12, Appl	323	27	48.2	411	6	US-11-061-869-12	Sequence 12, Appl
251	28	50.0	1593	7	US-11-149-003-4	Sequence 4, Appl	324	27	48.2	411	6	US-10-821-234-989	Sequence 16, Appl
252	28	50.0	1628	7	US-11-149-003-2	Sequence 2, Appl	325	27	48.2	413	6	US-10-821-234-989	Sequence 989, App
253	28	50.0	1637	6	US-10-821-234-1204	Sequence 1204, Ap	326	27	48.2	418	7	US-11-072-512-2420	Sequence 2420, Ap
254	28	50.0	2050	6	US-10-453-372-192	Sequence 192, App	327	27	48.2	419	7	US-11-171-531-2	Sequence 2, Appl
255	28	50.0	2280	7	US-11-022-562-211	Sequence 211, App	328	27	48.2	436	7	US-11-024-959-394	Sequence 394, App
256	28	50.0	2715	7	US-11-096-051-2	Sequence 2, Appl	329	27	48.2	447	7	US-11-049-348-6	Sequence 6, Appl
257	28	50.0	2715	7	US-11-113-424-51	Sequence 51, Appl	330	27	48.2	453	7	US-11-150-888-2	Sequence 2, Appl
258	28	50.0	2721	7	US-11-096-051-10	Sequence 10, Appl	331	27	48.2	458	6	US-10-878-556A-28	Sequence 28, Appl
259	28	50.0	2725	7	US-11-096-051-8	Sequence 8, Appl	332	27	48.2	463	6	US-10-467-657-6352	Sequence 6352, Ap
260	28	50.0	3597	7	US-11-019-711-6	Sequence 6, Appl	333	27	48.2	463	6	US-10-467-657-7604	Sequence 7604, Ap
261	28	50.0	3600	7	US-11-019-711-2	Sequence 2, Appl	334	27	48.2	465	6	US-10-467-657-5040	Sequence 5040, Ap
262	28	50.0	3690	6	US-10-995-561-1016	Sequence 1016, Ap	335	27	48.2	472	6	US-10-508-263-62	Sequence 62, Appl
263	28	50.0	3714	6	US-10-995-561-1015	Sequence 1015, Ap	336	27	48.2	472	6	US-10-508-263-64	Sequence 64, Appl
264	28	50.0	3717	6	US-10-821-234-1076	Sequence 1076, Ap	337	27	48.2	473	6	US-10-508-263-14	Sequence 23, Appl
265	27.5	49.1	261	6	US-10-821-234-930	Sequence 930, App	338	27	48.2	485	7	US-11-072-512-3419	Sequence 3419, Ap
266	27.5	49.1	273	5	US-09-978-360A-709	Sequence 709, App	339	27	48.2	488	6	US-10-508-263-12	Sequence 12, Appl
267	27	48.2	50	7	US-11-000-463-919	Sequence 919, App	340	27	48.2	489	6	US-10-467-657-6054	Sequence 6054, Ap
268	27	48.2	51	6	US-10-467-657-1244	Sequence 1244, Ap	341	27	48.2	490	6	US-10-508-263-10	Sequence 10, Appl
269	27	48.2	58	6	US-10-467-657-3262	Sequence 3262, Ap	342	27	48.2	491	7	US-11-098-662-14	Sequence 14, Appl
270	27	48.2	58	6	US-10-467-657-6856	Sequence 6856, Ap	343	27	48.2	491	7	US-11-165-141-2	Sequence 2, Appl
271	27	48.2	101	7	US-11-072-512-2117	Sequence 2117, Ap	344	27	48.2	493	7	US-11-098-686-10233	Sequence 10233, A
272	27	48.2	104	7	US-11-072-512-2466	Sequence 2466, Ap	345	27	48.2	496	6	US-10-508-263-14	Sequence 14, Appl
273	27	48.2	105	6	US-10-986-501-112	Sequence 112, App	346	27	48.2	496	7	US-11-182-016-33	Sequence 33, Appl
274	27	48.2	105	6	US-10-821-234-1149	Sequence 1149, Ap	347	27	48.2	500	7	US-11-012-668-4	Sequence 4, Appl
275	27	48.2	106	6	US-10-821-234-1191	Sequence 1191, Ap	348	27	48.2	511	7	US-11-012-762-48	Sequence 48, Appl
276	27	48.2	106	7	US-11-072-512-2364	Sequence 2364, Ap	349	27	48.2	512	7	US-11-012-762-64	Sequence 64, Appl
277	27	48.2	112	6	US-10-678-790-62	Sequence 62, Appl	350	27	48.2	513	6	US-10-467-657-5464	Sequence 5464, Ap
278	27	48.2	119	7	US-11-174-150-41	Sequence 41, Appl	351	27	48.2	520	7	US-11-098-662-12	Sequence 12, Appl
279	27	48.2	126	7	US-11-113-424-184	Sequence 184, App	352	27	48.2	520	7	US-11-165-141-19	Sequence 19, Appl
280	27	48.2	127	7	US-11-072-512-2861	Sequence 2861, Ap	353	27	48.2	522	7	US-11-193-955-11	Sequence 11, Appl
281	27	48.2	127	7	US-11-072-512-2875	Sequence 2875, Ap	354	27	48.2	522	7	US-11-184-399-8	Sequence 8, Appl
282	27	48.2	127	7	US-11-072-512-3032	Sequence 3032, Ap	355	27	48.2	535	6	US-10-793-626-1024	Sequence 1024, Ap
283	27	48.2	148	7	US-11-147-047-30	Sequence 30, Appl	356	27	48.2	545	6	US-10-063-703-110	Sequence 110, App
284	27	48.2	155	7	US-11-072-512-3331	Sequence 3331, Ap	357	27	48.2	545	7	US-11-102-240-110	Sequence 110, App
285	27	48.2	158	7	US-11-072-512-3610	Sequence 3610, Ap	358	27	48.2	548	6	US-10-493-909-77	Sequence 77, Appl
286	27	48.2	159	7	US-11-147-047-29	Sequence 29, Appl	359	27	48.2	548	6	US-10-493-909-78	Sequence 78, Appl
287	27	48.2	173	6	US-10-821-234-1291	Sequence 1291, Ap	360	27	48.2	548	7	US-11-137-465-47	Sequence 47, Appl
288	27	48.2	201	7	US-11-057-012-4	Sequence 4, Appl	361	27	48.2	550	7	US-11-185-342-14	Sequence 14, Appl
289	27	48.2	203	7	US-11-165-141-4	Sequence 4, Appl	362	27	48.2	559	6	US-10-821-234-1513	Sequence 1513, Ap
290	27	48.2	205	6	US-10-689-742-72	Sequence 72, Appl	363	27	48.2	567	7	US-11-049-348-5	Sequence 5, Appl
291	27	48.2	211	7	US-11-098-662-16	Sequence 16, Appl	364	27	48.2	590	7	US-11-131-212-73	Sequence 73, Appl
292	27	48.2	211	7	US-11-165-141-21	Sequence 21, Appl	365	27	48.2	599	7	US-11-165-141-33	Sequence 33, Appl
293	27	48.2	211	7	US-11-072-512-3219	Sequence 3219, Ap	366	27	48.2	600	7	US-11-205-109-39	Sequence 39, Appl
294	27	48.2	213	7	US-11-072-512-2657	Sequence 2657, Ap	367	27	48.2	602	7	US-11-072-512-3324	Sequence 3324, Ap
295	27	48.2	216	7	US-11-072-512-3032	Sequence 3032, Ap	368	27	48.2	604	6	US-10-453-372-1160	Sequence 1160, Ap
296	27	48.2	229	6	US-10-131-826A-178	Sequence 178, App	369	27	48.2	611	7	US-11-049-348-4	Sequence 4, Appl
297	27	48.2	229	6	US-10-467-657-916	Sequence 916, App	370	27	48.2	611	7	US-11-010-239-129	Sequence 129, App
298	27	48.2	233	7	US-11-098-686-10888	Sequence 10888, A	371	27	48.2	616	6	US-10-858-730-21	Sequence 21, Appl
299	27	48.2	243	6	US-10-511-538-81	Sequence 81, Appl	372	27	48.2	650	7	US-11-119-249-7	Sequence 7, Appl
300	27	48.2	244	7	US-11-184-399-10	Sequence 10, Appl	373	27	48.2	664	6	US-10-793-626-346	Sequence 346, App
301	27	48.2	252	7	US-11-098-686-10367	Sequence 10367, A	374	27	48.2	679	6	US-11-072-512-2774	Sequence 2774, Ap
302	27	48.2	260	7	US-11-098-686-11143	Sequence 11143, A	375	27	48.2	713	6	US-10-467-657-762	Sequence 762, App
303	27	48.2	269	6	US-10-821-234-1684	Sequence 1684, Ap	376	27	48.2	748	7	US-11-150-756-2	Sequence 2, Appl
304	27	48.2	275	6	US-10-523-477-10	Sequence 10, Appl	377	27	48.2	776	6	US-10-453-372-44	Sequence 44, Appl
305	27	48.2	299	6	US-10-967-671-13	Sequence 13, Appl	378	27	48.2	833	7	US-10-453-372-46	Sequence 46, Appl
306	27	48.2	307	7	US-11-019-711-90	Sequence 90, Appl	379	27	48.2	858	6	US-11-159-902-2	Sequence 2, Appl
307	27	48.2	312	7	US-11-197-721-14	Sequence 14, Appl	380	27	48.2	858	6	US-10-645-441-25	Sequence 25, Appl
308	27	48.2	333	6	US-10-980-388-91	Sequence 91, Appl	381	27	48.2	882	6	US-10-725-475-4	Sequence 4, Appl
309	27	48.2	333	6	US-10-980-388-114	Sequence 114, App	382	27	48.2	882	6	US-10-453-372-60	Sequence 60, Appl
310	27	48.2	333	7	US-11-050-440-2	Sequence 2, Appl	383	27	48.2	884	6	US-10-453-372-58	Sequence 58, Appl
311	27	48.2	336	7	US-11-197-721-10	Sequence 10, Appl	384	27	48.2	937	6	US-11-057-058-55	Sequence 55, Appl
312	27	48.2	339	6	US-10-821-234-1085	Sequence 1085, Ap	385	27	48.2	974	6	US-10-995-561-895	Sequence 895, App
313	27	48.2	342	7	US-11-072-512-2201	Sequence 2201, Ap	386	27	48.2	997	6	US-10-995-561-896	Sequence 896, App
314	27	48.2	353	7	US-11-098-686-10774	Sequence 10774, A	387	27	48.2	1236	6	US-10-912-971-8	Sequence 8, Appl
315	27	48.2	358	6	US-10-770-726-60	Sequence 60, Appl	388	27	48.2	1236	7	US-11-080-991-68	Sequence 68, Appl
316	27	48.2	363	6	US-10-995-561-541	Sequence 541, App	389	27	48.2	1238	7	US-11-078-735-21	Sequence 21, Appl
317	27	48.2	374	7	US-11-057-012-51	Sequence 51, Appl	390	27	48.2	1238	7	US-11-050-346-66	Sequence 66, Appl

391	27	48.2	1238	7	US-11-103-077-21	Sequence 21, Appl	464	26	46.4	339	6	US-10-995-561-682	Sequence 682, App
392	27	48.2	1402	6	US-10-971-982-2	Sequence 2, Appl	465	26	46.4	339	6	US-10-995-561-684	Sequence 684, App
393	27	48.2	1519	7	US-11-182-016-5	Sequence 19, Appl	466	26	46.4	339	6	US-10-995-561-685	Sequence 685, App
394	27	48.2	1730	7	US-11-182-016-19	Sequence 5, Appl	466	26	46.4	339	6	US-10-995-561-686	Sequence 686, App
395	27	48.2	1907	7	US-11-039-398-25	Sequence 25, Appl	468	26	46.4	339	6	US-10-995-561-687	Sequence 687, App
396	27	48.2	2011	7	US-11-080-931-56	Sequence 56, Appl	469	26	46.4	339	7	US-11-186-284-43	Sequence 43, Appl
397	27	48.2	3353	7	US-11-037-243-64	Sequence 64, Appl	470	26	46.4	339	7	US-11-185-877-11	Sequence 11, Appl
398	27	48.2	3635	7	US-11-019-711-47	Sequence 47, Appl	471	26	46.4	343	6	US-11-080-091-4	Sequence 4, Appl
399	27	48.2	3748	7	US-11-132-686-8	Sequence 8, Appl	472	26	46.4	344	6	US-10-821-234-923	Sequence 923, App
400	27	48.2	3749	7	US-11-132-686-6	Sequence 6, Appl	473	26	46.4	345	7	US-11-087-177-19	Sequence 19, Appl
401	27	48.2	3749	7	US-11-132-686-12	Sequence 12, Appl	474	26	46.4	345	7	US-11-087-177-21	Sequence 21, Appl
402	27	48.2	3912	7	US-11-132-686-7	Sequence 7, Appl	475	26	46.4	353	6	US-10-131-826A-296	Sequence 296, App
403	27	48.2	3913	7	US-11-132-686-5	Sequence 5, Appl	476	26	46.4	353	7	US-11-012-762-50	Sequence 50, Appl
404	27	48.2	3913	7	US-11-132-686-9	Sequence 9, Appl	477	26	46.4	357	7	US-11-120-368-188	Sequence 188, App
405	26.5	47.3	529	6	US-10-467-657-1502	Sequence 1502, Ap	478	26	46.4	362	7	US-11-012-762-62	Sequence 62, Appl
406	26.5	47.3	529	6	US-11-122-144-2	Sequence 2, Appl	479	26	46.4	362	7	US-11-080-091-12	Sequence 12, Appl
407	26	46.4	14	7	US-11-093-724B-16	Sequence 16, Appl	480	26	46.4	368	6	US-11-072-512-3645	Sequence 3645, Ap
408	26	46.4	31	6	US-10-895-064-1381	Sequence 1381, Ap	481	26	46.4	378	6	US-10-793-626-1428	Sequence 1428, Ap
409	26	46.4	48	7	US-11-123-896-303	Sequence 303, App	482	26	46.4	379	7	US-11-012-522-7	Sequence 7, Appl
410	26	46.4	57	6	US-10-467-657-3928	Sequence 3928, Ap	483	26	46.4	389	6	US-10-523-674-42	Sequence 42, Appl
411	26	46.4	64	7	US-11-123-896-117	Sequence 117, App	484	26	46.4	404	7	US-11-052-554A-322	Sequence 322, App
412	26	46.4	64	7	US-11-123-896-120	Sequence 120, App	485	26	46.4	406	6	US-10-493-909-68	Sequence 68, Appl
413	26	46.4	75	7	US-11-123-896-116	Sequence 116, App	486	26	46.4	406	7	US-11-107-028-7	Sequence 7, Appl
414	26	46.4	75	7	US-11-123-896-119	Sequence 119, App	487	26	46.4	421	6	US-10-453-372-220	Sequence 220, App
415	26	46.4	75	7	US-11-123-896-302	Sequence 302, App	488	26	46.4	424	7	US-11-024-959-499	Sequence 499, App
416	26	46.4	82	7	US-11-000-463-743	Sequence 743, App	489	26	46.4	436	7	US-11-124-368A-236	Sequence 236, App
417	26	46.4	82	7	US-11-000-463-744	Sequence 744, App	490	26	46.4	448	7	US-11-112-882-64	Sequence 64, Appl
418	26	46.4	83	6	US-10-510-386-114	Sequence 114, App	491	26	46.4	448	7	US-11-112-882-65	Sequence 65, Appl
419	26	46.4	86	7	US-11-055-822-748	Sequence 748, App	492	26	46.4	448	7	US-11-112-882-66	Sequence 66, Appl
420	26	46.4	93	7	US-11-000-463-272	Sequence 272, App	493	26	46.4	449	7	US-11-112-882-70	Sequence 70, Appl
421	26	46.4	109	7	US-11-072-512-3476	Sequence 3476, Ap	494	26	46.4	449	7	US-11-112-882-71	Sequence 71, Appl
422	26	46.4	111	6	US-10-063-703-130	Sequence 130, App	495	26	46.4	458	7	US-11-112-882-69	Sequence 69, Appl
423	26	46.4	111	6	US-11-102-240-130	Sequence 130, App	496	26	46.4	459	6	US-11-112-882-68	Sequence 68, Appl
424	26	46.4	117	7	US-11-000-463-271	Sequence 271, App	497	26	46.4	459	7	US-10-724-598-16	Sequence 16, Appl
425	26	46.4	119	6	US-10-821-234-1044	Sequence 1044, Ap	498	26	46.4	470	7	US-11-143-984A-31	Sequence 31, Appl
426	26	46.4	132	7	US-11-234-786-573	Sequence 573, App	499	26	46.4	471	6	US-10-770-726-68	Sequence 68, Appl
427	26	46.4	135	7	US-11-098-686-11098	Sequence 11098, A	500	26	46.4	471	7	US-10-770-726-68	Sequence 68, Appl
428	26	46.4	140	7	US-11-124-367A-455	Sequence 455, App	501	26	46.4	473	7	US-11-152-366-31	Sequence 31, Appl
429	26	46.4	143	7	US-11-234-786-482	Sequence 482, App	502	26	46.4	481	7	US-11-152-366-32	Sequence 32, Appl
430	26	46.4	153	6	US-10-821-234-1355	Sequence 1355, Ap	503	26	46.4	482	6	US-11-094-519A-27	Sequence 27, Appl
431	26	46.4	156	7	US-11-055-822-744	Sequence 744, App	504	26	46.4	482	6	US-10-689-742-66	Sequence 66, Appl
432	26	46.4	164	7	US-11-124-367A-453	Sequence 453, App	505	26	46.4	484	6	US-10-995-561-560	Sequence 560, App
433	26	46.4	164	7	US-11-124-367A-454	Sequence 454, App	506	26	46.4	485	6	US-10-091-342-8	Sequence 8, Appl
434	26	46.4	164	7	US-11-124-367A-454	Sequence 454, App	506	26	46.4	485	6	US-10-485-517-136	Sequence 136, App
435	26	46.4	165	7	US-11-072-512-3099	Sequence 3099, Ap	507	26	46.4	487	6	US-10-980-722-2	Sequence 2, Appl
436	26	46.4	165	7	US-11-176-830-2	Sequence 2, Appl	508	26	46.4	503	6	US-10-980-722-2	Sequence 2, Appl
437	26	46.4	176	7	US-11-128-059-72	Sequence 72, Appl	509	26	46.4	516	6	US-11-019-711-104	Sequence 104, App
438	26	46.4	190	7	US-11-093-118-16	Sequence 16, Appl	511	26	46.4	516	6	US-10-091-342-10	Sequence 10, Appl
439	26	46.4	200	6	US-10-467-657-5256	Sequence 5256, Ap	512	26	46.4	527	6	US-10-995-561-559	Sequence 559, App
440	26	46.4	202	6	US-10-467-657-16	Sequence 16, Appl	513	26	46.4	527	6	US-11-135-604-2	Sequence 2, Appl
441	26	46.4	202	6	US-10-467-657-5648	Sequence 5648, Ap	514	26	46.4	532	7	US-11-135-604-4	Sequence 4, Appl
442	26	46.4	208	6	US-10-055-877-186	Sequence 186, App	515	26	46.4	533	6	US-10-453-372-230	Sequence 230, App
443	26	46.4	208	6	US-11-072-512-2520	Sequence 2520, Ap	516	26	46.4	533	6	US-10-453-372-232	Sequence 232, App
444	26	46.4	216	6	US-10-821-234-984	Sequence 984, App	517	26	46.4	537	7	US-11-135-604-6	Sequence 6, Appl
445	26	46.4	219	6	US-10-714-887-152	Sequence 152, App	518	26	46.4	537	7	US-11-135-604-6	Sequence 6, Appl
446	26	46.4	232	7	US-11-128-059-66	Sequence 66, Appl	519	26	46.4	552	6	US-10-453-372-234	Sequence 234, App
447	26	46.4	232	7	US-10-453-372-214	Sequence 214, App	520	26	46.4	552	6	US-10-453-372-236	Sequence 236, App
448	26	46.4	255	7	US-11-120-368-98	Sequence 98, Appl	521	26	46.4	552	6	US-10-453-372-238	Sequence 238, App
449	26	46.4	264	7	US-11-119-769-6	Sequence 6, Appl	522	26	46.4	552	6	US-10-453-372-240	Sequence 240, App
450	26	46.4	292	7	US-11-129-143-95	Sequence 95, Appl	523	26	46.4	552	6	US-10-453-372-242	Sequence 242, App
451	26	46.4	292	7	US-11-080-091-9	Sequence 9, Appl	524	26	46.4	552	6	US-10-453-372-244	Sequence 244, App
452	26	46.4	299	7	US-11-072-512-2792	Sequence 2792, Ap	525	26	46.4	552	6	US-10-453-372-246	Sequence 246, App
453	26	46.4	304	7	US-11-080-091-10	Sequence 10, Appl	526	26	46.4	552	6	US-10-453-372-248	Sequence 248, App
454	26	46.4	311	5	US-09-978-318B-31	Sequence 31, Appl	527	26	46.4	552	6	US-10-453-372-250	Sequence 250, App
455	26	46.4	311	7	US-11-072-512-3429	Sequence 3429, Ap	528	26	46.4	554	6	US-11-000-463-240	Sequence 240, App
456	26	46.4	315	6	US-10-453-372-212	Sequence 212, App	529	26	46.4	556	6	US-10-453-372-210	Sequence 210, App
457	26	46.4	329	7	US-11-098-686-10153	Sequence 10153, A	530	26	46.4	562	6	US-10-995-561-561	Sequence 561, App
458	26	46.4	332	6	US-10-131-826A-386	Sequence 386, App	531	26	46.4	562	7	US-11-169-041-153	Sequence 153, App
459	26	46.4	337	6	US-10-980-388-115	Sequence 115, App	532	26	46.4	562	7	US-11-183-205-26	Sequence 26, Appl
460	26	46.4	337	6	US-10-063-703-74	Sequence 74, Appl	533	26	46.4	562	7	US-11-072-512-2310	Sequence 2310, Ap
461	26	46.4	337	7	US-11-103-240-74	Sequence 74, Appl	534	26	46.4	574	6	US-10-453-372-226	Sequence 226, App
462	26	46.4	339	6	US-10-878-556A-18	Sequence 18, Appl	535	26	46.4	597	7	US-11-045-802-28	Sequence 28, Appl
463	26	46.4	339	6	US-10-995-561-681	Sequence 681, App	536	26	46.4	599	7	US-11-109-157A-3	Sequence 3, Appl

537	26	46.4	617	6	US-10-995-561-890	Sequence 890, App	610	26	46.4	2417	6	US-10-453-372-228	Sequence 228, App
538	26	46.4	619	7	US-11-019-711-34	Sequence 34, Appl	611	26	46.4	2439	7	US-11-128-059-76	Sequence 76, Appl
539	26	46.4	620	7	US-11-072-512-2045	Sequence 2045, Ap	612	26	46.4	2455	7	US-11-186-999-4	Sequence 4, Appl
540	26	46.4	651	7	US-11-194-246-342	Sequence 342, App	613	26	46.4	2458	7	US-11-128-059-94	Sequence 94, Appl
541	26	46.4	669	6	US-10-453-372-216	Sequence 216, App	614	26	46.4	2458	7	US-11-186-999-6	Sequence 6, Appl
542	26	46.4	669	6	US-10-453-372-218	Sequence 218, App	615	26	46.4	2458	7	US-11-186-999-11	Sequence 11, Appl
543	26	46.4	670	6	US-10-995-561-528	Sequence 528, App	616	26	46.4	2458	7	US-11-186-999-13	Sequence 13, Appl
544	26	46.4	687	7	US-11-117-169-6	Sequence 6, Appl	617	26	46.4	2515	7	US-11-113-424-53	Sequence 53, Appl
545	26	46.4	692	7	US-11-045-802-26	Sequence 26, Appl	618	26	46.4	2551	6	US-10-453-372-256	Sequence 256, App
546	26	46.4	710	7	US-11-078-189-18	Sequence 18, Appl	619	26	46.4	2551	6	US-11-128-059-96	Sequence 96, Appl
547	26	46.4	720	6	US-10-495-662-22	Sequence 22, Appl	620	26	46.4	3568	6	US-10-453-372-194	Sequence 194, App
548	26	46.4	721	7	US-11-128-059-88	Sequence 88, Appl	621	26	46.4	3570	6	US-10-453-372-178	Sequence 178, App
549	26	46.4	727	7	US-11-117-169-8	Sequence 8, Appl	622	26	46.4	3570	6	US-10-453-372-196	Sequence 196, App
550	26	46.4	733	7	US-11-012-762-68	Sequence 68, Appl	623	26	46.4	3570	6	US-10-453-372-198	Sequence 198, App
551	26	46.4	751	7	US-11-012-762-26	Sequence 26, Appl	624	26	46.4	3570	6	US-10-453-372-200	Sequence 200, App
552	26	46.4	753	6	US-10-858-730-225	Sequence 225, App	625	26	46.4	3570	6	US-10-453-372-202	Sequence 202, App
553	26	46.4	755	6	US-10-517-939-330	Sequence 330, App	626	26	46.4	3570	6	US-10-453-372-204	Sequence 204, App
554	26	46.4	759	7	US-11-072-512-2770	Sequence 2770, Ap	627	26	46.4	3570	6	US-10-453-372-206	Sequence 206, App
555	26	46.4	790	6	US-10-495-662-21	Sequence 21, Appl	628	26	46.4	3655	7	US-11-075-185-5	Sequence 5, Appl
556	26	46.4	791	6	US-10-495-662-20	Sequence 20, Appl	629	26	46.4	3716	7	US-11-052-554A-141	Sequence 141, App
557	26	46.4	818	7	US-11-072-512-2546	Sequence 2546, Ap	630	26	46.4	5935	6	US-10-995-561-776	Sequence 776, App
558	26	46.4	829	6	US-10-512-109-27	Sequence 27, Appl	631	25.5	45.5	55	6	US-10-467-657-8732	Sequence 8732, Ap
559	26	46.4	832	6	US-10-512-109-29	Sequence 29, Appl	632	25.5	45.5	118	7	US-11-020-772-13	Sequence 13, Appl
560	26	46.4	871	7	US-11-109-157A-10	Sequence 10, Appl	633	25.5	45.5	118	7	US-11-076-728-13	Sequence 13, Appl
561	26	46.4	882	7	US-11-098-686-10893	Sequence 10893, A	634	25.5	45.5	325	7	US-11-063-343-29	Sequence 29, Appl
562	26	46.4	889	7	US-11-072-512-3449	Sequence 3449, Ap	635	25.5	45.5	447	6	US-10-858-730-107	Sequence 107, App
563	26	46.4	897	6	US-10-453-372-208	Sequence 208, App	636	25.5	45.5	638	6	US-10-995-561-536	Sequence 536, App
564	26	46.4	924	6	US-10-857-780-20	Sequence 20, Appl	637	25.5	45.5	638	7	US-11-054-281-30	Sequence 30, Appl
565	26	46.4	924	6	US-10-493-909-67	Sequence 67, Appl	638	25.5	45.5	638	7	US-11-054-281-111	Sequence 111, App
566	26	46.4	924	7	US-11-107-028-26	Sequence 26, Appl	639	25.5	45.5	638	7	US-11-054-281-112	Sequence 112, App
567	26	46.4	931	7	US-11-128-059-86	Sequence 86, Appl	640	25.5	45.5	643	7	US-11-054-281-113	Sequence 113, App
568	26	46.4	937	7	US-11-098-686-11296	Sequence 11296, A	641	25.5	45.5	4913	6	US-10-453-372-1142	Sequence 1142, Ap
569	26	46.4	1046	7	US-11-120-308-186	Sequence 186, App	642	25.5	45.5	4961	6	US-10-453-372-1132	Sequence 1132, Ap
570	26	46.4	1096	6	US-10-995-561-710	Sequence 710, App	643	25	44.6	9	7	US-11-040-159-132	Sequence 122, App
571	26	46.4	1103	7	US-11-109-157A-9	Sequence 9, Appl	644	25	44.6	14	7	US-11-054-515-2796	Sequence 2796, Ap
572	26	46.4	1133	6	US-10-821-234-1219	Sequence 1219, Ap	645	25	44.6	17	6	US-10-895-064-2745	Sequence 2745, Ap
573	26	46.4	1141	7	US-11-072-512-2522	Sequence 2522, Ap	646	25	44.6	21	7	US-11-233-683-28	Sequence 28, Appl
574	26	46.4	1162	6	US-10-451-375-3	Sequence 3, Appl	647	25	44.6	32	6	US-10-467-657-2568	Sequence 2568, Ap
575	26	46.4	1198	6	US-10-451-375-4	Sequence 4, Appl	648	25	44.6	35	7	US-11-055-163-3	Sequence 3, Appl
576	26	46.4	1210	6	US-10-624-932-26	Sequence 26, Appl	649	25	44.6	35	7	US-11-233-683-50	Sequence 50, Appl
577	26	46.4	1213	7	US-11-039-398-14	Sequence 14, Appl	650	25	44.6	35	7	US-11-233-683-55	Sequence 55, Appl
578	26	46.4	1216	7	US-11-039-398-12	Sequence 12, Appl	651	25	44.6	38	7	US-11-069-856-24	Sequence 24, Appl
579	26	46.4	1219	7	US-11-039-398-10	Sequence 10, Appl	652	25	44.6	41	7	US-11-233-683-30	Sequence 30, Appl
580	26	46.4	1222	7	US-11-039-398-8	Sequence 8, Appl	653	25	44.6	41	7	US-11-233-683-35	Sequence 35, Appl
581	26	46.4	1232	7	US-11-039-398-18	Sequence 18, Appl	654	25	44.6	41	7	US-11-233-683-36	Sequence 36, Appl
582	26	46.4	1235	7	US-11-039-398-16	Sequence 16, Appl	655	25	44.6	41	7	US-11-233-683-37	Sequence 37, Appl
583	26	46.4	1249	7	US-11-039-398-22	Sequence 22, Appl	656	25	44.6	41	7	US-11-233-683-44	Sequence 44, Appl
584	26	46.4	1250	7	US-11-137-465-62	Sequence 62, Appl	657	25	44.6	41	7	US-11-233-683-47	Sequence 47, Appl
585	26	46.4	1252	7	US-11-039-398-20	Sequence 20, Appl	658	25	44.6	42	6	US-10-924-074-15	Sequence 15, Appl
586	26	46.4	1302	6	US-10-995-561-1024	Sequence 1024, Ap	659	25	44.6	47	6	US-11-000-463-756	Sequence 756, App
587	26	46.4	1323	7	US-11-128-059-92	Sequence 92, Appl	660	25	44.6	48	6	US-10-467-657-738	Sequence 738, App
588	26	46.4	1327	7	US-11-128-059-84	Sequence 84, Appl	661	25	44.6	48	6	US-10-467-657-746	Sequence 746, App
589	26	46.4	1375	6	US-10-995-561-809	Sequence 809, App	662	25	44.6	48	6	US-10-467-657-838	Sequence 838, App
590	26	46.4	1377	6	US-10-821-234-1070	Sequence 1070, Ap	663	25	44.6	48	6	US-10-467-657-870	Sequence 870, App
591	26	46.4	1416	7	US-11-128-059-4	Sequence 4, Appl	664	25	44.6	50	6	US-10-467-657-1262	Sequence 1262, Ap
592	26	46.4	1502	6	US-10-453-372-252	Sequence 252, App	665	25	44.6	52	6	US-10-924-074-13	Sequence 13, Appl
593	26	46.4	1510	6	US-10-453-372-254	Sequence 254, App	666	25	44.6	52	7	US-11-233-683-29	Sequence 29, Appl
594	26	46.4	1649	6	US-10-995-561-974	Sequence 974, App	667	25	44.6	52	7	US-11-233-683-34	Sequence 34, Appl
595	26	46.4	1686	7	US-11-109-157A-1	Sequence 1, Appl	668	25	44.6	54	7	US-11-133-949-7	Sequence 7, Appl
596	26	46.4	1686	7	US-11-226-701-2	Sequence 2, Appl	669	25	44.6	55	6	US-10-467-657-1086	Sequence 1086, Ap
597	26	46.4	1694	7	US-11-135-855-36	Sequence 36, Appl	670	25	44.6	57	6	US-10-467-657-7378	Sequence 7378, Ap
598	26	46.4	1700	6	US-10-453-372-398	Sequence 398, App	671	25	44.6	73	5	US-09-978-360A-578	Sequence 578, App
599	26	46.4	1700	6	US-10-453-372-412	Sequence 412, App	672	25	44.6	73	6	US-10-467-657-898	Sequence 898, App
600	26	46.4	1700	6	US-10-453-372-414	Sequence 414, App	673	25	44.6	75	6	US-10-895-064-1481	Sequence 1481, Ap
601	26	46.4	1700	6	US-10-453-372-416	Sequence 416, App	674	25	44.6	82	7	US-11-020-772-8	Sequence 8, Appl
602	26	46.4	1700	6	US-10-453-372-418	Sequence 418, App	675	25	44.6	82	7	US-11-076-728-8	Sequence 8, Appl
603	26	46.4	1709	6	US-10-995-561-973	Sequence 973, App	676	25	44.6	87	7	US-11-093-118-30	Sequence 30, Appl
604	26	46.4	1709	6	US-10-453-372-410	Sequence 410, App	677	25	44.6	87	7	US-11-031-206-130	Sequence 130, App
605	26	46.4	1709	7	US-11-135-855-35	Sequence 35, Appl	678	25	44.6	91	6	US-10-821-234-1103	Sequence 1103, Ap
606	26	46.4	1866	7	US-11-126-313-32	Sequence 32, Appl	679	25	44.6	91	6	US-10-505-263-72	Sequence 72, Appl
607	26	46.4	2086	7	US-11-128-059-82	Sequence 82, Appl	680	25	44.6	111	6	US-10-821-234-1178	Sequence 1178, Ap
608	26	46.4	2313	7	US-11-128-059-80	Sequence 80, Appl	681	25	44.6	111	7	US-11-072-512-2298	Sequence 2298, Ap
609	26	46.4	2358	7	US-11-128-059-74	Sequence 74, Appl	682	25	44.6	112	7	US-11-072-512-2298	Sequence 7, Appl

683	25	44.6	112	7	US-11-076-728-7	Sequence 7, Appli	756	25	44.6	256	7	US-11-039-003-14	Sequence 14, Appli
684	25	44.6	116	6	US-10-467-657-354	Sequence 354, App	757	25	44.6	258	6	US-10-467-657-3202	Sequence 3202, Ap
685	25	44.6	118	6	US-10-467-657-4296	Sequence 4296, Ap	758	25	44.6	259	6	US-10-495-662-24	Sequence 24, Appli
686	25	44.6	119	6	US-10-467-657-5916	Sequence 5916, Ap	759	25	44.6	259	6	US-10-821-234-1561	Sequence 1561, Ap
687	25	44.6	120	5	US-09-978-360A-465	Sequence 465, App	760	25	44.6	259	6	US-10-055-877-225	Sequence 225, App
688	25	44.6	125	7	US-11-093-118-12	Sequence 12, Appli	761	25	44.6	259	6	US-10-055-877-237	Sequence 237, App
689	25	44.6	125	7	US-11-072-512-2369	Sequence 2369, Ap	762	25	44.6	259	7	US-11-037-923-6	Sequence 6, Appli
690	25	44.6	129	6	US-10-967-527A-13	Sequence 13, Appli	763	25	44.6	267	6	US-10-841-956A-4	Sequence 4, Appli
691	25	44.6	129	7	US-11-072-512-2669	Sequence 2669, Ap	764	25	44.6	267	6	US-10-055-877-36	Sequence 36, Appli
692	25	44.6	144	7	US-11-234-786-480	Sequence 480, App	765	25	44.6	267	6	US-10-055-877-38	Sequence 38, Appli
693	25	44.6	145	7	US-11-072-512-3910	Sequence 3910, Ap	766	25	44.6	269	6	US-10-841-956A-8	Sequence 8, Appli
694	25	44.6	148	6	US-10-467-657-5478	Sequence 5478, Ap	767	25	44.6	270	6	US-10-841-956A-5	Sequence 5, Appli
695	25	44.6	150	6	US-10-895-084-1189	Sequence 1189, Ap	768	25	44.6	271	6	US-10-467-657-2266	Sequence 2266, App
696	25	44.6	155	6	US-11-072-512-3937	Sequence 3937, Ap	769	25	44.6	277	6	US-10-055-877-236	Sequence 236, App
697	25	44.6	156	7	US-11-072-512-2055	Sequence 2055, Ap	770	25	44.6	281	6	US-10-841-956A-7	Sequence 7, Appli
698	25	44.6	158	7	US-11-072-512-3047	Sequence 3047, Ap	771	25	44.6	282	6	US-10-841-956A-6	Sequence 6, Appli
699	25	44.6	161	6	US-10-623-155-114	Sequence 114, App	772	25	44.6	287	7	US-11-057-012-43	Sequence 43, Appli
700	25	44.6	162	5	US-09-978-360A-464	Sequence 464, App	773	25	44.6	289	6	US-10-793-626-1120	Sequence 1120, Ap
701	25	44.6	162	6	US-10-453-372-876	Sequence 876, App	774	25	44.6	292	6	US-10-965-972-6	Sequence 6, Appli
702	25	44.6	165	7	US-11-176-830-7	Sequence 7, Appli	775	25	44.6	296	6	US-10-841-956A-9	Sequence 9, Appli
703	25	44.6	165	7	US-11-196-067-7	Sequence 7, Appli	776	25	44.6	296	6	US-10-965-972-8	Sequence 8, Appli
704	25	44.6	169	5	US-09-978-360A-720	Sequence 720, App	777	25	44.6	296	6	US-10-954-468-9	Sequence 9, Appli
705	25	44.6	169	7	US-11-120-318-1	Sequence 1, Appli	778	25	44.6	297	7	US-11-072-512-2441	Sequence 2441, Ap
706	25	44.6	170	6	US-10-055-877-50	Sequence 50, Appli	779	25	44.6	300	6	US-10-923-232B-62	Sequence 62, Appli
707	25	44.6	170	6	US-10-453-372-888	Sequence 888, App	780	25	44.6	301	6	US-10-467-657-7356	Sequence 7356, Ap
708	25	44.6	170	6	US-10-453-372-888	Sequence 888, App	781	25	44.6	301	6	US-10-877-346-73	Sequence 73, Appli
709	25	44.6	170	6	US-11-072-512-2785	Sequence 2785, Ap	782	25	44.6	302	7	US-11-156-084-345	Sequence 345, App
710	25	44.6	172	6	US-10-821-234-1588	Sequence 1588, Ap	783	25	44.6	303	7	US-11-186-284-193	Sequence 193, App
711	25	44.6	173	6	US-10-453-372-862	Sequence 862, App	784	25	44.6	317	7	US-11-156-084-197	Sequence 197, App
712	25	44.6	180	7	US-11-176-830-731	Sequence 731, Appli	785	25	44.6	317	7	US-11-156-084-256	Sequence 256, App
713	25	44.6	180	7	US-11-176-830-732	Sequence 732, App	786	25	44.6	317	7	US-11-156-084-257	Sequence 257, App
714	25	44.6	181	7	US-11-031-206-132	Sequence 132, App	787	25	44.6	317	7	US-11-156-084-295	Sequence 295, App
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716	25	44.6	203	6	US-11-069-856-1	Sequence 1, Appli	789	25	44.6	318	6	US-10-329-258-2	Sequence 2, Appli
717	25	44.6	204	6	US-10-055-877-161	Sequence 161, App	790	25	44.6	320	7	US-11-183-205-50	Sequence 50, Appli
718	25	44.6	208	7	US-11-072-512-3920	Sequence 3920, Ap	791	25	44.6	322	6	US-10-793-626-270	Sequence 270, App
719	25	44.6	210	7	US-11-213-359-3	Sequence 3, Appli	792	25	44.6	323	6	US-10-525-674-8	Sequence 8, Appli
720	25	44.6	211	7	US-11-090-878-46	Sequence 46, Appli	793	25	44.6	325	6	US-11-088-686-10585	Sequence 10585, A
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852	25	44.6	326	7	US-11-102-621-63	Sequence 63, Appl	925	25	44.6	376	7	US-11-012-762-22	Sequence 22, Appl
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863	25	44.6	328	6	US-10-131-826A-326	Sequence 326, Appl	936	25	44.6	381	6	US-10-525-674-20	Sequence 20, Appl
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866	25	44.6	330	6	US-10-886-303-6	Sequence 6, Appl	939	25	44.6	382	7	US-11-012-762-52	Sequence 52, Appl
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871	25	44.6	330	7	US-11-075-351-1	Sequence 1, Appl	944	25	44.6	391	6	US-10-467-657-2524	Sequence 2524, Ap
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877	25	44.6	330	7	US-11-102-621-69	Sequence 69, Appl	950	25	44.6	400	6	US-10-948-053-5	Sequence 5, Appl
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881	25	44.6	330	7	US-11-102-621-76	Sequence 76, Appl	954	25	44.6	402	7	US-11-024-251-31	Sequence 31, Appl
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883	25	44.6	330	7	US-11-124-620-1	Sequence 1, Appl	956	25	44.6	406	6	US-10-453-372-188	Sequence 188, Ap
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891	25	44.6	342	6	US-10-689-742-218	Sequence 218, Appl	964	25	44.6	415	7	US-11-029-003-12	Sequence 12, Appl
892	25	44.6	344	7	US-11-055-163-8	Sequence 8, Appl	965	25	44.6	419	6	US-10-821-234-1504	Sequence 1504, Ap
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ALIGNMENTS

RESULT 1
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 ; Sequence 2358, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 2358
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2358

Query Match 92.9%; Score 52; DB 6; Length 257;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 134 MALPPCHAL 142

RESULT 2
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 ; Sequence 990, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompejus, Markus
 ; APPLICANT: Kroger, Burkhard
 ; APPLICANT: Schroder, Hartwig
 ; APPLICANT: Zelzer, Oskar

APPLICANT: Haberhauer, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121CPCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; CURRENT FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 990
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-055-822-990

Query Match 83.9%; Score 47; DB 7; Length 225;
 Best Local Similarity 88.9%; Pred. No. 0.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MALPPCHAL 10
 |||||
 Db 144 MALPPCHLL 152

RESULT 3
 US-11-165-067A-28
 ; Sequence 28, Application US/11165067A
 ; Publication No. US20060014257A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KATASHKINA Joanna Yosifovna
 ; APPLICANT: SKOROKHOVA Aleksandra Yurievna
 ; APPLICANT: ZIMENKOV Danila Vadimovich
 ; APPLICANT: GULEVICH Andrey Yurievich
 ; APPLICANT: ERRAIS Lopes Lubov
 ; APPLICANT: BIRYUKOVA Irina Vladimirovna
 ; APPLICANT: MIRONOV Aleksandr Sergeevich
 ; APPLICANT: MASHKO Sergei Vladimirovich
 ; TITLE OF INVENTION: RSF1010 DERIVATIVE Mob- PLASMID CONTAINING NO ANTIBIOTIC RESISTAN
 ; FILE REFERENCE: US-174
 ; CURRENT APPLICATION NUMBER: US/11/165,067A
 ; CURRENT FILING DATE: 2005-06-24
 ; PRIOR APPLICATION NUMBER: RU2004119027
 ; PRIOR FILING DATE: 2004-06-24
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 28
 ; LENGTH: 264
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-11-165-067A-28

Query Match 71.4%; Score 40; DB 7; Length 264;
 Best Local Similarity 87.5%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHA 9
Db 141 MALAPCHA 148

RESULT 4

US-11-165-067A-45
; Sequence 45, Application US/11165067A
; Publication No. US20060014257A1
; GENERAL INFORMATION:
; APPLICANT: KATASHKINA Joanna Yosifovna
; APPLICANT: SKOROKHOVA Aleksandra Yurievna
; APPLICANT: ZIMENKOV Danila Vadimovich
; APPLICANT: GULEVICH Andrey Yurievich
; APPLICANT: ERRAIS Lopes Lubov
; APPLICANT: BIRUKOVA Irina Vladimirovna
; APPLICANT: MIRONOV Aleksandr Sergeevich
; APPLICANT: MASHKO Sergei Vladimirovich
; TITLE OF INVENTION: RS1010 DERIVATIVE Mob- PLASMID CONTAINING NO ANTIBIOTIC RESISTANCE
; FILE REFERENCE: US-174
; CURRENT APPLICATION NUMBER: US/11/165,067A
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: RU2004119027
; PRIOR FILING DATE: 2004-06-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-165-067A-45

Query Match 71.4%; Score 40; DB 7; Length 264;

Best Local Similarity 87.5%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHA 9
Db 141 MALAPCHA 148

RESULT 5

US-11-184-005-5
; Sequence 5, Application US/11184005
; Publication No. US20050256052A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank P.
; APPLICANT: Moos, Malcolm JR.
; APPLICANT: Hoang, Bang
; APPLICANT: Wang, Shouwen
; TITLE OF INVENTION: METHOD OF MODULATING TISSUE
; FILE REFERENCE: NIH133.1CPC3
; CURRENT APPLICATION NUMBER: US/11/184,005
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US 10/028051
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 08/822333
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: US 08/729,452
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-184-005-5

Query Match 64.3%; Score 36; DB 7; Length 111;

Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
Db 68 ALPPCRSL 75

RESULT 6

US-10-821-234-1023
; Sequence 1023, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1023
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1023

Query Match 62.5%; Score 35; DB 6; Length 232;

Best Local Similarity 60.0%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
Db 52 LLPCPPCRAL 61

RESULT 7

US-11-072-512-2358
; Sequence 2358, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1

```
; SEQ ID NO 2358
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2358

Query Match      60.7%; Score 34; DB 7; Length 111;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 PPCHAL 10
Db      90 PPCHRL 95

RESULT 8
US-11-068-783-112
; Sequence 112, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 66081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 112
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Trimeresurus wagleri
US-11-068-783-112

Query Match      58.9%; Score 33; DB 7; Length 23;
Best Local Similarity 80.0%; Pred. No. 6;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LPPCH 8
Db      11 IPPCH 15

RESULT 9
US-10-353-783-52
; Sequence 52, Application US/10353783
; Publication No. US20050261175A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Kristina M.
; APPLICANT: Bosseiman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/353,783
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,729
; FILING DATE: 24-MAY-1995
; APPLICATION NUMBER: 08/172,329
; FILING DATE: 21-DEC-1993
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; APPLICATION NUMBER: 07/684,535
; FILING DATE: 10-APR-1991
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/32958A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-353-783-52

Query Match      58.9%; Score 33; DB 6; Length 271;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LMALPPCHAL 10
Db      215 VMALPACFSL 224

RESULT 10
US-11-169-041-233
; Sequence 233, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-233

Query Match      58.9%; Score 33; DB 7; Length 296;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCH 8
Db      :||| |||
```

Db 88 LALAPCH 94

RESULT 11

US-11-131-035-2
; Sequence 2, Application US/11131035
; Publication No. US20060019341A1
; GENERAL INFORMATION:
; APPLICANT: JOLY, John C.
; TITLE OF INVENTION: AMINOPEPTIDASE
; FILE REFERENCE: P1920R1
; CURRENT APPLICATION NUMBER: US/11/131,035
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/243,789
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,350
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-131-035-2

Query Match 58.9%; Score 33; DB 7; Length 688;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10

Db 153 MFLPGCHRL 161

RESULT 12

US-11-067-811-1
; Sequence 1, Application US/11067811
; Publication No. US20050260688A1
; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A.
; APPLICANT: Enshell-Sciffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; LENGTH: 1042
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-811-1

Query Match 58.9%; Score 33; DB 7; Length 1042;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LPPCHAL 10

Db 526 IPPCRAL 532

RESULT 13

US-11-124-367A-388
; Sequence 388, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD

; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-388

Query Match 58.9%; Score 33; DB 7; Length 1047;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 LMALPP--CHA 9

Db 118 LMALPTTICHA 128

RESULT 14

US-11-124-367A-386
; Sequence 386, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Hongjin Huang
; APPLICANT: Michele Cargill
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 1058
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-386

Query Match 58.9%; Score 33; DB 7; Length 1058;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 LMALPP--CHA 9

Db 129 LMALPTTICHA 139

RESULT 15

US-11-124-367A-387
; Sequence 387, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846

; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 387
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-387

Query Match 58.9%; Score 33; DB 7; Length 1062;
Best Local Similarity 72.7%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 LMALPP-CHA 9
Db 133 LMALPTTICHA 143

RESULT 16
US-11-072-512-2662
; Sequence 2662, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2662
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2662

Query Match 57.1%; Score 32; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PCHAL 10
Db 58 PCHAL 62

RESULT 17
US-11-072-512-2271
; Sequence 2271, Application US/11072512

; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2271
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2271

Query Match 57.1%; Score 32; DB 7; Length 145;
Best Local Similarity 71.4%; Pred. No. 49;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMALPPC 7
Db 59 LLLPPC 65

RESULT 18
US-10-995-561-824
; Sequence 824, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 824
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-824

Query Match 57.1%; Score 32; DB 6; Length 191;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMALPPC 7
Db 141 ILSLPPC 147

```
RESULT 19
US-10-995-561-823
; Sequence 823, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 823
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-823

Query Match 57.1%; Score 32; DB 6; Length 236;
Best Local Similarity 57.1%; Pred. No. 77;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMAIPLPC 7
DB 186 ILSLPPC 192

RESULT 20
US-10-523-038-5
; Sequence 5, Application US/10523038
; Publication No. US20050287648A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Harold
; APPLICANT: SOWDEN, Mark P.
; APPLICANT: DEWHURST, Stephen
; APPLICANT: KIM, Baek
; APPLICANT: WEDEKIND, Joseph
; TITLE OF INVENTION: PROTEIN TRANSDUCING DOMAIN/DEAMINASE
; FILE REFERENCE: 21108.0034U2
; CURRENT APPLICATION NUMBER: US/10/523,038
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: PCT/US03/24458
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 60/419,982
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/401,293
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
US-10-523-038-5

Query Match 57.1%; Score 32; DB 6; Length 236;
Best Local Similarity 57.1%; Pred. No. 77;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMAIPLPC 7
DB 186 ILSLPPC 192

RESULT 21
US-10-523-038-45
; Sequence 45, Application US/10523038
; Publication No. US20050287648A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Harold
; APPLICANT: SOWDEN, Mark P.
; APPLICANT: DEWHURST, Stephen
; APPLICANT: KIM, Baek
; APPLICANT: WEDEKIND, Joseph
; TITLE OF INVENTION: CHIMERIC PROTEINS, RELATED COMPOUNDS, AND USES THEREOF
; FILE REFERENCE: 21108.0034U2
; CURRENT APPLICATION NUMBER: US/10/523,038
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: PCT/US03/24458
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: 60/419,982
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/401,293
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note =
US-10-523-038-45

Query Match 57.1%; Score 32; DB 6; Length 237;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMAIPLPC 7
DB 187 ILSLPPC 193

RESULT 22
US-10-131-826A-34
; Sequence 34, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
```

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 34
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-826A-34

Query Match          57.1%; Score 32; DB 6; Length 328;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 MALPPCH 8
      | :|||:
Db      239 MTIPCY 245

RESULT 23
US-10-995-561-892
; Sequence 892, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 892
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-892

Query Match          57.1%; Score 32; DB 6; Length 391;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
      | :|||:
Db      8 LAGKPKCHAL 17

RESULT 24
US-10-995-561-893
; Sequence 893, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 893
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-893

Query Match          57.1%; Score 32; DB 6; Length 391;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
      | :|||:
Db      8 LAGKPKCHAL 17

RESULT 25
US-11-169-041-158
; Sequence 158, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 158
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-158

Query Match          57.1%; Score 32; DB 7; Length 400;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 LPPCHAL 10
      | :|||:
Db      218 LPPAHAI 224

RESULT 26
US-10-880-764-3
; Sequence 3, Application US/10880764
; Publication No. US2006000335A1
; GENERAL INFORMATION:
; APPLICANT: John D. Crispino
; TITLE OF INVENTION: METHODS FOR DIAGNOSING ACUTE MEGAKARYOBLASTIC LEUKEMIA
; FILE REFERENCE: 27373/38893A
; CURRENT APPLICATION NUMBER: US/10/880,764
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/483,954
; PRIOR FILING DATE: 2003-07-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-880-764-3

Query Match          57.1%; Score 32; DB 6; Length 413;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 MALPPCHA 9
      | :|||:
      | :|||:
```

Db 194 LPLPCEA 201

RESULT 27

US-10-986-501-110
; Sequence 110, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 110
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (169)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-986-501-110

Query Match 57.1%; Score 32; DB 6; Length 457;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCHA 9
Db 76 PPCHS 80

RESULT 28

US-11-072-512-3794
; Sequence 3794, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAHOKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3794
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3794

Query Match 57.1%; Score 32; DB 7; Length 482;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCHA 9
Db 76 PPCHS 80

RESULT 29

US-10-667-295-201
; Sequence 201, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(486)
; OTHER INFORMATION: Ceres Seq. ID no. 12349431
US-10-667-295-201

Query Match 57.1%; Score 32; DB 6; Length 486;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ALPPCH 8
Db 27 APPCH 32

RESULT 30

US-11-072-512-2580
; Sequence 2580, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2580
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2580

Query Match 57.1%; Score 32; DB 7; Length 510;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCHA 9
DB 204 PPCHS 208

RESULT 31
US-10-972-053-2
; Sequence 2, Application US/10972053
; Publication No. US20050255489A1
; GENERAL INFORMATION:
; APPLICANT: Pierce, James Michael
; APPLICANT: Kamar, Maria
; APPLICANT: Lee, Jin-Kyu
; TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant
; TITLE OF INVENTION: Cells and Methods
; FILE REFERENCE: 49-02A
; CURRENT APPLICATION NUMBER: US/10/972,053
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US03/091402
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,172
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-053-2

Query Match 57.1%; Score 32; DB 6; Length 782;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10

DB 672 AWPPAHAL 679

RESULT 32

US-10-972-053-8
; Sequence 8, Application US/10972053
; Publication No. US20050255489A1
; GENERAL INFORMATION:
; APPLICANT: Pierce, James Michael
; APPLICANT: Kamar, Maria
; APPLICANT: Lee, Jin-Kyu
; APPLICANT: Kaneko, Mika
; TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant
; TITLE OF INVENTION: Cells and Methods
; FILE REFERENCE: 49-02A
; CURRENT APPLICATION NUMBER: US/10/972,053
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US03/091402
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,172
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-053-8

Query Match 57.1%; Score 32; DB 6; Length 782;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
DB 672 AWPPAHAL 679

RESULT 33
US-10-972-053-10
; Sequence 10, Application US/10972053
; Publication No. US20050255489A1
; GENERAL INFORMATION:
; APPLICANT: Pierce, James Michael
; APPLICANT: Kamar, Maria
; APPLICANT: Lee, Jin-Kyu
; APPLICANT: Kaneko, Mika
; TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant
; TITLE OF INVENTION: Cells and Methods
; FILE REFERENCE: 49-02A
; CURRENT APPLICATION NUMBER: US/10/972,053
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US03/091402
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,172
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-053-10

Query Match 57.1%; Score 32; DB 6; Length 784;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ALPPCHAL 10
DB 674 AWPPAHAL 681


```
RESULT 34
US-10-972-053-12
; Sequence 12, Application US/10972053
; Publication No. US20050255489A1
; GENERAL INFORMATION:
; APPLICANT: Pierce, James Michael
; APPLICANT: Kamar, Maria
; APPLICANT: Lee, Jin-Kyu
; APPLICANT: Kaneko, Mika
; TITLE OF INVENTION: N-Acetylglucosaminyltransferase Vb Coding Sequences, Recombinant
; TITLE OF INVENTION: Cells and Methods
; FILE REFERENCE: 49-02A
; CURRENT APPLICATION NUMBER: US/10/972,053
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US03/091402
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 60/375,172
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-972-053-12

Query Match          57.1%; Score 32; DB 6; Length 792;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ALPPCHAL 10
DB      682 AMPPAHAL 689

RESULT 35
US-11-072-512-2532
; Sequence 2532, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAL, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2532
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-11-072-512-2532

```
Query Match          57.1%; Score 32; DB 7; Length 869;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
DB      707 LEQLKPCCHGL 716

RESULT 36
US-11-183-624-2
; Sequence 2, Application US/11183624
; Publication No. US20050255518A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MPI01-272P1RM
; CURRENT APPLICATION NUMBER: US/11/183,624
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/281,866
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-183-624-2

Query Match          57.1%; Score 32; DB 7; Length 921;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LMALPPC 7
DB      12 LLAAAPC 18

RESULT 37
US-11-012-762-70
; Sequence 70, Application US/11012762
; Publication No. US20050244815A1
; GENERAL INFORMATION:
; APPLICANT: Georgia State University Research Foundation, Inc.
; TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes
; FILE REFERENCE: GSUI.PCT
; CURRENT APPLICATION NUMBER: US/11/012,762
; CURRENT FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/US03/19300
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/390,046
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-012-762-70

Query Match          57.1%; Score 32; DB 7; Length 1137;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 ALPPCHAL 10
DB      675 ALPPAYAL 682
```

```
RESULT 38
US-11-198-847-336
; Sequence 336, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 336
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Conus generalis
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Xaa may be Phe (D or L)
; NAME/KEY: DISULFID
; LOCATION: (4)..(14)
US-11-198-847-336

Query Match      55.4%; Score 31; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPCH 8
DB      12 PPCH 15

RESULT 39
US-11-198-847-337
; Sequence 337, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 337
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Conus generalis
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Xaa may be Phe (D or L)
; NAME/KEY: DISULFID
; LOCATION: (4)..(14)
US-11-198-847-337

Query Match      55.4%; Score 31; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPCH 8
DB      12 PPCH 15

RESULT 40
US-11-198-847-334
; Sequence 334, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 334
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Conus generalis
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (4)..(14)
US-11-198-847-334

Query Match      55.4%; Score 31; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPCH 8
DB      12 PPCH 15

RESULT 41
US-11-198-847-335
; Sequence 335, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Xaa may be Phe (D or L)
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(14)
US-11-198-847-337

Query Match      55.4%; Score 31; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPCH 8
DB      12 PPCH 15

RESULT 40
US-11-198-847-334
; Sequence 334, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 334
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Conus generalis
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (4)..(14)
US-11-198-847-334

Query Match      55.4%; Score 31; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PPCH 8
DB      12 PPCH 15

RESULT 41
US-11-198-847-335
; Sequence 335, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
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; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 335
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Conus generalis
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (6)..(14)
US-11-198-847-235

Query Match 55.4%; Score 31; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCH 8
|||
DB 12 PPCH 15

RESULT 42
US-11-198-847-235
; Sequence 235, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Conus generalis
US-11-198-847-235

Query Match 55.4%; Score 31; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCH 8
|||
DB 16 PPCH 19

RESULT 43
US-11-198-847-236
; Sequence 236, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.

; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; CURRENT FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Conus vexillum
US-11-198-847-236

Query Match 55.4%; Score 31; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPCH 8
|||
DB 16 PPCH 19

RESULT 44
US-11-120-308-92
; Sequence 92, Application US/11120308
; Publication No. US20060005277A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: cDNAs Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 92
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-120-308-92

Query Match 55.4%; Score 31; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPP 6

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Db          43 LMAUPP 48
|||||
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45
US-11-198-847-14
; Sequence 14, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus generalis
US-11-198-847-14

Query Match          55.4%; Score 31; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 PPCH 8
          |||||
Db          67 PPCH 70

RESULT 46
US-11-198-847-221
; Sequence 221, Application US/11198847
; Publication No. US20050271589A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Jones, Robert M.
; APPLICANT: Garrett, James E.
; APPLICANT: Watkins, Maren
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: B-Superfamily Conotoxins
; FILE REFERENCE: 2314-296
; CURRENT APPLICATION NUMBER: US/11/198,847
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: US 10/838,226
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 10/058,053
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/264323
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 221
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus vexillum
US-11-198-847-221

Query Match          55.4%; Score 31; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 PPCH 8
          |||||
Db          67 PPCH 70

RESULT 47
US-10-498-026-27
; Sequence 27, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Felis domesticus
US-10-498-026-27

Query Match          55.4%; Score 31; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 ALPPC 7
          |||||
Db          5 ALPPC 9

RESULT 48
US-11-033-039-135
; Sequence 135, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Felis catus
US-11-033-039-135

Query Match          55.4%; Score 31; DB 7; Length 88;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 ALPPC 7
          |||||
Db          5 ALPPC 9

RESULT 49
US-11-072-512-3765
; Sequence 3765, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
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; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3765
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3765
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Query Match          55.4%; Score 31; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      5 PPCH 8
Db      90 PPCH 93
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RESULT 50
US-11-072-512-2406
; Sequence 2406, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
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; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2406
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2406

Query Match          55.4%; Score 31; DB 7; Length 125;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      4 LPPCHAL 10
Db      42 LPPAHS 48

Search completed: February 17, 2006, 02:48:29
Job time : 21 secs
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OM protein - protein search, using sw model

Run on: February 17, 2006, 02:44:41 ; Search time 165 Seconds
(without alignments)
25.323 Million cell updates/sec

Title: US-10-734-049b-188

Perfect score: 56

Sequence: 1 LMALPPCHAL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

- Published Applications AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	56	100.0	10	5	US-10-734-049A-188
2	56	100.0	18	4	US-10-629-313-146
3	56	100.0	18	4	US-10-629-313-150
4	56	100.0	216	5	US-10-450-763-51128
5	56	100.0	313	4	US-10-308-192-5
6	56	100.0	313	4	US-10-629-313-142
7	56	100.0	313	5	US-10-733-878-433
8	56	100.0	313	5	US-10-723-860-1171
9	56	100.0	313	5	US-10-734-049A-267
10	56	100.0	313	5	US-10-756-149-4996
11	52	92.9	264	4	US-10-282-122A-66040
12	52	92.9	264	4	US-10-282-122A-66163
13	52	92.9	266	4	US-10-282-122A-65128
14	49	87.5	314	4	US-10-282-122A-61012
15	48	85.7	109	4	US-10-424-599-247816
16	48	85.7	154	4	US-10-424-599-247814
17	48	85.7	263	4	US-10-282-122A-64769
18	48	85.7	266	4	US-10-282-122A-61802
19	48	85.7	266	4	US-10-282-122A-62695
20	48	85.7	266	4	US-10-282-122A-63877
21	48	85.7	314	4	US-10-282-122A-45383
22	48	85.7	315	5	US-10-501-282-1160
23	48	85.7	321	6	US-11-097-143-5883
24	48	85.7	333	5	US-10-779-597-23
25	48	85.7	350	4	US-10-320-797-3118
26	48	85.7	530	4	US-10-424-599-247813
27	48	85.7	530	4	US-10-424-599-247817

28	48	85.7	579	4	US-10-425-114-49649	Sequence 49649, A
29	47	83.9	266	3	US-09-954-197-2	Sequence 2, Appl1
30	47	83.9	266	3	US-09-738-626-4442	Sequence 4442, Ap
31	47	83.9	279	4	US-10-282-122A-53671	Sequence 53671, A
32	47	83.9	323	4	US-10-282-122A-50921	Sequence 50921, A
33	47	83.9	323	4	US-10-282-122A-67673	Sequence 67673, A
34	47	83.9	323	4	US-10-282-122A-69408	Sequence 69408, A
35	46	83.1	55	5	US-10-958-216-469	Sequence 469, App
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38	46	82.1	315	5	US-10-958-216-464	Sequence 464, App
39	46	82.1	315	5	US-10-958-216-466	Sequence 466, App
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42	46	82.1	318	4	US-10-282-122A-70811	Sequence 70811, A
43	46	82.1	318	4	US-10-282-122A-71845	Sequence 71845, A
44	46	82.1	318	5	US-10-857-625-654	Sequence 654, App
45	44	78.6	51	3	US-09-855-604-277	Sequence 277, App
46	44	78.6	51	3	US-09-855-604-277	Sequence 277, App
47	44	78.6	93	3	US-09-864-408A-6614	Sequence 6614, Ap
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49	44	78.6	136	3	US-09-867-550-396	Sequence 396, App
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51	44	78.6	184	3	US-09-870-725-2	Sequence 2, Appl1
52	44	78.6	184	4	US-10-295-027-173	Sequence 173, App
53	44	78.6	184	4	US-10-188-832-47	Sequence 47, Appl
54	44	78.6	196	4	US-10-437-963-129581	Sequence 129581, A
55	44	78.6	280	4	US-10-282-122A-45156	Sequence 45156, A
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57	44	78.6	315	4	US-10-032-585-7236	Sequence 7236, Ap
58	44	78.6	328	4	US-10-282-122A-64240	Sequence 64240, A
59	44	78.6	340	4	US-10-083-357-1337	Sequence 1337, Ap
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62	44	78.6	523	4	US-10-425-115-295501	Sequence 295501, A
63	44	78.6	584	4	US-10-437-963-139579	Sequence 139579, A
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79	40	71.4	264	4	US-10-282-122A-78362	Sequence 78362, A
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87	39	63.6	223	4	US-10-425-115-344248	Sequence 344248, A
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93	38	67.9	127	3	US-09-867-550-762	Sequence 762, App
94	38	67.9	147	5	US-10-450-763-57751	Sequence 57751, A
95	38	67.9	395	4	US-10-389-647-528	Sequence 528, App
96	38	67.9	1101	4	US-10-259-194A-28	Sequence 28, Appl
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131	36	64.3	111	4	US-10-028-051-5	Sequence 5, Appl	204	35	62.5	159	4	US-10-296-115-1476	Sequence 1476, Ap
132	36	64.3	111	4	US-10-014-055-5	Sequence 5, Appl	205	35	62.5	173	4	US-10-437-963-185043	Sequence 185043,
133	36	64.3	111	4	US-10-090-049-5	Sequence 5, Appl	206	35	62.5	174	4	US-10-425-115-241690	Sequence 241690,
134	36	64.3	111	4	US-10-437-963-170063	Sequence 170063,	207	35	62.5	186	4	US-10-425-115-191821	Sequence 191821,
135	36	64.3	112	4	US-10-138-434A-16	Sequence 16, Appl	208	35	62.5	186	4	US-10-425-115-213286	Sequence 213286,
136	36	64.3	120	3	US-09-738-626-6323	Sequence 6323, Ap	209	35	62.5	195	4	US-10-094-749-3275	Sequence 3275, Ap
137	36	64.3	130	4	US-10-437-963-145261	Sequence 145261,	210	35	62.5	196	4	US-10-853-386-104	Sequence 104, App
138	36	64.3	135	4	US-10-437-963-119773	Sequence 119773,	211	35	62.5	196	4	US-10-295-027-158	Sequence 158, App
139	36	64.3	142	4	US-10-425-115-338926	Sequence 338926,	212	35	62.5	196	4	US-10-188-832-29	Sequence 29, Appl
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143	36	64.3	166	4	US-10-425-115-267763	Sequence 267763,	216	35	62.5	239	4	US-10-425-115-284905	Sequence 284905,
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154	36	64.3	544	3	US-09-847-102A-40	Sequence 40, Appl	227	35	62.5	352	4	US-10-292-798-1802	Sequence 1802, Ap
155	36	64.3	626	3	US-09-847-102A-45	Sequence 45, Appl	228	35	62.5	353	4	US-10-233-553-29	Sequence 29, Appl
156	36	64.3	635	4	US-09-847-102A-44	Sequence 44, Appl	229	35	62.5	353	4	US-10-684-422-308	Sequence 308, App
157	36	64.3	647	3	US-10-282-122A-78520	Sequence 78520, A	230	35	62.5	353	5	US-10-437-963-104785	Sequence 104785,
158	36	64.3	647	5	US-10-285-976-39	Sequence 39, Appl	231	35	62.5	363	4	US-10-437-963-6820	Sequence 6820, Ap
159	36	64.3	647	5	US-10-287-436A-466	Sequence 466, App	232	35	62.5	377	4	US-10-425-115-263599	Sequence 263599,
160	36	64.3	647	5	US-10-287-436A-598	Sequence 598, App	233	35	62.5	384	5	US-10-425-115-263599	Sequence 2865, Ap
161	36	64.3	680	4	US-10-287-436A-1163	Sequence 1163, Ap	234	35	62.5	388	5	US-10-732-923-2865	Sequence 123148,
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165	36	64.3	888	4	US-10-210-130-94	Sequence 94, Appl	238	35	62.5	530	4	US-10-437-963-146485	Sequence 146485,
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167	36	64.3	1057	4	US-10-437-963-175037	Sequence 175037,	240	35	62.5	557	6	US-11-097-143-15603	Sequence 15603, A
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169	36	64.3	4601	6	US-11-097-143-4905	Sequence 4905, Ap	242	35	62.5	586	5	US-10-732-923-1838	Sequence 1838, Ap
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172	35	62.5	62	4	US-10-437-963-143214	Sequence 143214,	245	35	62.5	611	4	US-10-424-599-173518	Sequence 173518,
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249	35	62.5	764	4	US-10-437-963-110724	Sequence 110724, A	322	34	60.7	253	3	US-09-847-102A-71	Sequence 71, Appl
250	35	62.5	839	4	US-10-399-456-11	Sequence 11, Appl	323	34	60.7	257	4	US-10-437-963-114368	Sequence 114368, A
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252	35	62.5	891	5	US-10-732-923-14985	Sequence 14985, A	325	34	60.7	287	3	US-09-897-214-11	Sequence 11, Appl
253	35	62.5	930	4	US-10-437-963-157595	Sequence 157595, A	326	34	60.7	287	3	US-09-893-737-110	Sequence 110, Appl
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261	35	62.5	4660	4	US-10-464-368-74	Sequence 74, Appl	334	34	60.7	346	5	US-10-732-923-9874	Sequence 9874, Ap
262	35	62.5	5374	4	US-10-028-248A-75	Sequence 75, Appl	335	34	60.7	365	5	US-10-773-236-295	Sequence 295, Ap
263	35	62.5	5374	4	US-10-107-782-75	Sequence 75, Appl	336	34	60.7	411	4	US-10-094-749-1666	Sequence 1666, Ap
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265	35	62.5	5376	4	US-10-107-782-74	Sequence 74, Appl	338	34	60.7	420	4	US-10-112-944-735	Sequence 735, App
266	35	62.5	5376	4	US-10-107-782-74	Sequence 74, Appl	339	34	60.7	430	4	US-10-437-963-200942	Sequence 200942, A
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273	34	60.7	62	4	US-10-424-599-158260	Sequence 158260, A	346	34	60.7	572	3	US-09-847-102A-55	Sequence 55, Appl
274	34	60.7	65	3	US-09-910-009A-357	Sequence 357, App	347	34	60.7	572	3	US-10-146-474-13	Sequence 13, Appl
275	34	60.7	65	4	US-10-828-478-357	Sequence 357, App	348	34	60.7	572	4	US-10-301-764-13	Sequence 13, Appl
276	34	60.7	67	4	US-10-424-599-155071	Sequence 155071, A	349	34	60.7	573	4	US-10-152-548-14	Sequence 14, Appl
277	34	60.7	70	3	US-09-864-761-41852	Sequence 41852, A	350	34	60.7	574	3	US-09-847-102A-54	Sequence 54, Appl
278	34	60.7	74	4	US-10-036-542-109	Sequence 109, App	351	34	60.7	574	4	US-10-285-976-51	Sequence 51, Appl
279	34	60.7	74	4	US-10-424-599-213650	Sequence 213650, A	352	34	60.7	574	5	US-10-723-860-1079	Sequence 1079, Ap
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283	34	60.7	84	4	US-10-425-115-233969	Sequence 233969, A	356	34	60.7	650	5	US-10-732-923-22495	Sequence 22495, A
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285	34	60.7	86	4	US-10-425-115-193105	Sequence 193105, A	358	34	60.7	693	4	US-10-087-192-1065	Sequence 1065, Ap
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294	34	60.7	112	4	US-10-264-237-2476	Sequence 2476, Ap	367	34	60.7	945	4	US-10-333-314-15	Sequence 15, Appl
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296	34	60.7	121	4	US-10-425-115-198999	Sequence 198999, A	369	34	60.7	976	3	US-09-801-368-248	Sequence 248, App
297	34	60.7	124	4	US-10-437-963-110981	Sequence 110981, A	370	34	60.7	976	4	US-10-149-310-182	Sequence 182, App
298	34	60.7	127	4	US-10-425-115-242532	Sequence 242532, A	371	34	60.7	982	4	US-10-618-941-120	Sequence 120, App
299	34	60.7	138	4	US-10-437-963-175175	Sequence 175175, A	372	34	60.7	1000	4	US-10-139-092-10	Sequence 10, Appl
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315	34	60.7	217	4	US-10-437-963-109106	Sequence 109106, A	388	34	60.7	1597	5	US-10-930-723A-20	Sequence 20, Appl
316	34	60.7	218	4	US-10-425-115-347164	Sequence 347164, A	389	34	60.7	1597	5	US-10-927-951A-20	Sequence 20, Appl
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319	34	60.7	246	4	US-10-425-115-212689	Sequence 212689, A	392	33	58.9	23	3	US-09-030-619-231	Sequence 231, App

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337	33	58.9	38	4	US-10-424-599-148647	Sequence 148647, A	470	33	58.9	203	4	US-10-424-599-164053	Sequence 164053, A
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352	33	58.9	71	4	US-10-424-599-270573	Sequence 270573, A	485	33	58.9	271	4	US-10-175-608-52	Sequence 52, Appl
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356	33	58.9	82	3	US-09-925-297-815	Sequence 815, App	489	33	58.9	286	4	US-10-425-115-331145	Sequence 331145, A
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358	33	58.9	82	4	US-10-425-115-195931	Sequence 195931, A	491	33	58.9	291	4	US-10-425-115-320557	Sequence 320557, A
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368	33	58.9	99	4	US-10-767-701-36806	Sequence 36806, A	501	33	58.9	334	4	US-10-437-963-159550	Sequence 159550, A
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370	33	58.9	100	4	US-10-437-963-188286	Sequence 188286, A	503	33	58.9	368	3	US-09-397-945-317	Sequence 317, App
371	33	58.9	100	4	US-10-425-115-345927	Sequence 345927, A	504	33	58.9	368	4	US-10-653-595-317	Sequence 317, App
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376	33	58.9	106	4	US-10-437-963-136950	Sequence 136950, A	509	33	58.9	393	4	US-10-156-761-13952	Sequence 13952, A
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384	33	58.9	124	4	US-10-437-963-140281	Sequence 140281, A	517	33	58.9	468	3	US-09-833-245-2260	Sequence 2260, Ap
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389	33	58.9	130	4	US-10-425-115-230351	Sequence 230351, A	522	33	58.9	488	4	US-10-755-899-260	Sequence 260, Appl
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393	33	58.9	138	4	US-10-437-963-150203	Sequence 150203, A	526	33	58.9	498	4	US-10-852-335A-106	Sequence 106, App
394	33	58.9	139	4	US-10-425-115-209165	Sequence 209165, A	527	33	58.9	520	5	US-10-437-963-203241	Sequence 203241, A
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403	33	58.9	172	4	US-10-424-599-259762	Sequence 259762, A	536	33	58.9	601	4	US-10-437-963-119213	Sequence 119213, A
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544	33	58.9	685	4	US-10-259-194A-234	Sequence 234, App	617	32	57.1	87	4	US-10-425-115-277289	Sequence 277289,
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548	33	58.9	723	5	US-09-893-737-100	Sequence 100, App	621	32	57.1	89	4	US-10-425-115-308494	Sequence 308494,
549	33	58.9	723	5	US-10-970-713-100	Sequence 100, App	622	32	57.1	91	4	US-10-437-963-108267	Sequence 108267,
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553	33	58.9	778	4	US-10-093-463-192	Sequence 192, App	626	32	57.1	96	4	US-10-425-115-266085	Sequence 266085,
554	33	58.9	781	5	US-10-450-763-45097	Sequence 45097, A	627	32	57.1	96	4	US-10-437-963-157192	Sequence 157192,
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RESULT 1
US-10-734-049A-188
; Sequence 188, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyojo
; APPLICANT: SHICHIO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734,049A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/JPO2/05799
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001/177058
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001/250728
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed peptide recognized by HLA-A2 restricted cytotoxic T
; OTHER INFORMATION: lymphocytes
US-10-734-049A-188
```

```
Query Match 100.0%; Score 56; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 LMALPPCHAL 10
Db 1 LMALPPCHAL 10
```

```
RESULT 2
US-10-629-313-146
; Sequence 146, Application US/10629313
; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Hong Chen
```

```
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Allison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIP5
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-313-146

Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LMALPPCHAL 10
Db 3 LMALPPCHAL 12

RESULT 3
US-10-629-313-150
; Sequence 150, Application US/10629313
; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Hong Chen
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Allison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-18
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIP5
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-629-313-150

Query Match      100.0%; Score 56; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
Db      3 LMALPPCHAL 12

RESULT 4
US-10-450-763-51128
; Sequence 51128, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51128
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (133)...(182)
; OTHER INFORMATION: Thymidylate synthase proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00091E, p-value=9.813e-32, raw score of 22.23
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)...(216)
; OTHER INFORMATION: Thymidylate synthase domain identified by Pfam, accession
; OTHER INFORMATION: name thymidylat_synt, E-value=1.3e-68, Pfam score of 241.4
;
US-10-450-763-51128

Query Match      100.0%; Score 56; DB 5; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
Db      116 LMALPPCHAL 125

RESULT 5
US-10-308-192-5
; Sequence 5, Application US/10308192
; Publication No. US20030224985A1
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence
; APPLICANT: Werner, Geurtsen
; TITLE OF INVENTION: Novel Thymidylate Synthase Mutants
; FILE REFERENCE: 03100132aa
; CURRENT APPLICATION NUMBER: US/10/308,192
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
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```
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-308-192-5

Query Match      100.0%; Score 56; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
Db      189 LMALPPCHAL 198

RESULT 6
US-10-629-313-142
; Sequence 142, Application US/10629313
; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Hong Chen
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Alison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-1
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIP5
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-629-313-142

Query Match      100.0%; Score 56; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCHAL 10
Db      189 LMALPPCHAL 198

RESULT 7
US-10-733-878-433
; Sequence 433, Application US/10733878
; Publication No. US20040224408A1
; GENERAL INFORMATION:
; APPLICANT: Jean-Philippe Girard
; APPLICANT: Francois Amalric
; APPLICANT: Myriam Roussigne
; APPLICANT: Thomas Clouaife
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
; TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
```

; TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BIOBANK.012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-878-433

Query Match 100.0%; Score 56; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

RESULT 8

US-10-723-860-1171
; Sequence 1171, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1171
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1171

Query Match 100.0%; Score 56; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

RESULT 9

US-10-734-049A-267
; Sequence 267, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; APPLICANT: SHICHIGO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734,049A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/JP02/05799
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001/177058
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001/250728

; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 267
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-049A-267

Query Match 100.0%; Score 56; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

RESULT 10

US-10-756-149-4996
; Sequence 4996, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4996
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-4996

Query Match 100.0%; Score 56; DB 5; Length 313;
Best Local Similarity 100.0%; Pred. No. 0.69; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

Qy 1 LMALPPCHAL 10
Db 189 LMALPPCHAL 198

RESULT 11

US-10-282-122A-66040
; Sequence 66040, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 66040
;; LENGTH: 264
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-10-282-122A-66040

Query Match 92.9%; Score 52; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 141 MALPPCHAL 149

RESULT 12

US-10-282-122A-66163
;; Sequence 66163, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA 034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 66040
;; LENGTH: 264
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-10-282-122A-66040

;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 66163
;; LENGTH: 264
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66163

Query Match 92.9%; Score 52; DB 4; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
DB 141 MALPPCHAL 149

RESULT 13

US-10-282-122A-65128
;; Sequence 65128, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA 034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 65128
;; LENGTH: 266
;; TYPE: PRT
;; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65128

Query Match 92.9%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      2 MALPPCHAL 10
      |||||
Db      143 MALPPCHAL 151

RESULT 14
US-10-282-122A-61012
; Sequence 61012, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61012
; TYPE: PRT
; LENGTH: 314
; ORGANISM: Listeria monocytogenes
US-10-282-122A-61012

Query Match      87.5%; Score 49; DB 4; Length 314;
Best Local Similarity 88.9%; Pred. No. 8.8;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 MALPPCHAL 10
      |||||
Db      191 MALPPCHSL 199

RESULT 15
US-10-424-599-247816
; Sequence 247816, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247816
; TYPE: PRT
; LENGTH: 109
; ORGANISM: Glycine max
; APPLICANT: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(109)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65808C.1.pep
US-10-424-599-247816

Query Match      85.7%; Score 48; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCH 8
      |||||
Db      42 LMALPPCH 49

RESULT 16
US-10-424-599-247814
; Sequence 247814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247814
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(154)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65806C.1.pep
US-10-424-599-247814

Query Match      85.7%; Score 48; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LMALPPCH 8
      |||||
Db      30 LMALPPCH 37

RESULT 17
US-10-282-122A-64769
; Sequence 64769, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
```

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; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64769
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64769

Query Match      85.7%; Score 48; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 11;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MALPPCHA 9
Db      141 MALPPCHA 148
|||||

RESULT 18
US-10-282-122A-61802
; Sequence 61802, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64769
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64769

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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61802
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-61802

Query Match      85.7%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MALPPCHA 9
Db      144 MALPPCHA 151
|||||

RESULT 19
US-10-282-122A-62695
; Sequence 62695, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62695
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62695

Query Match      85.7%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MALPPCHA 9
Db      144 MALPPCHA 151

RESULT 20
US-10-282-122A-63877
; Sequence 63877, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63877
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63877

Query Match      85.7%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MALPPCHA 9
Db      144 MALPPCHA 151

RESULT 21
US-10-282-122A-45383
; Sequence 45383, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45383
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (136)..(136)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (293)..(293)
; OTHER INFORMATION: X=any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (293)..(293)
; OTHER INFORMATION: X=any amino acid
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-45383

Query Match      85.7%; Score 48; DB 4; Length 314;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 MALPPCHAL 10
| | | | | | | |
Db 191 MALPPCHTL 199

RESULT 22

US-10-501-282-1160
; Sequence 1160, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOON
; APPLICANT: ZAGURSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1160
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-1160

Query Match 85.7%; Score 48; DB 5; Length 315;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | | | |
Db 192 MALPPCHTL 200

RESULT 23

US-11-097-143-5883
; Sequence 5883, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5883
; LENGTH: 321
; TYPE: PRT

; ORGANISM: DROSOPHILA
US-11-097-143-5883

Query Match 85.7%; Score 48; DB 6; Length 321;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | | | |
Db 196 MALPPCHCL 204

RESULT 24

US-10-779-597-23
; Sequence 23, Application US/10779597
; Publication No. US20040234953A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Wong, Scott W.
; APPLICANT: Axthelm, Michael K.
; APPLICANT: Hansen, Scott G.
; TITLE OF INVENTION: JAPANESE MACAQUE HERPESVIRUS NUCLEIC ACID SEQUENCES AND THEIR USE
; FILE REFERENCE: 178-67426
; CURRENT APPLICATION NUMBER: US/10/779,597
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/276,524
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/16274
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205,652
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Japanese Macaque Herpesvirus
US-10-779-597-23

Query Match 85.7%; Score 48; DB 5; Length 333;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
| | | | | | | |
Db 210 MALPPCHVL 218

RESULT 25

US-10-320-797-3118
; Sequence 3118, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3118
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
; FEATURE:
; NAME/KEY: MISC_FEATURE

; LOCATION: (271)..(271)
; OTHER INFORMATION: Xaa = any amino acid
US-10-320-797-3118

Query Match 85.7%; Score 48; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8
|||||
DB 192 LMALPPCH 199

RESULT 26

US-10-424-599-247813
; Sequence 247813, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247813
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65805C.1.pep
US-10-424-599-247813

Query Match 85.7%; Score 48; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8
|||||
DB 406 LMALPPCH 413

RESULT 27

US-10-424-599-247817
; Sequence 247817, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247817
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65809C.1.pep
US-10-424-599-247817

Query Match 85.7%; Score 48; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8

DB 406 LMALPPCH 413
|||||

RESULT 28

US-10-425-114-49649
; Sequence 49649, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49649
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-050-G2_FLI.pep
US-10-425-114-49649

Query Match 85.7%; Score 48; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMALPPCH 8
|||||
DB 455 LMALPPCH 462

RESULT 29

US-09-954-197-2
; Sequence 2, Application US/09954197
; Patent No. US20020107379A1
; GENERAL INFORMATION:
; APPLICANT: MARX, Achim
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE thya GENE
; FILE REFERENCE: 032301 WD 201
; CURRENT APPLICATION NUMBER: US/09/954,197
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-954-197-2

Query Match 83.9%; Score 47; DB 3; Length 266;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
|||||
DB 144 MALPPCHLL 152

RESULT 30

US-09-738-626-4442
; Sequence 4442, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO

APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4442
LENGTH: 266
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4442

Query Match 83.9%; Score 47; DB 3; Length 266;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 MALPPCHAL 10
DB 144 MALPPCHLL 152

RESULT 31

US-10-282-122A-53671
Sequence 53671, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50921
LENGTH: 323
TYPE: PRT
ORGANISM: Bordetella pertussis
US-10-282-122A-50921

Query Match 83.9%; Score 47; DB 4; Length 323;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53671
LENGTH: 279
TYPE: PRT
ORGANISM: Corynebacterium diphtheriae
US-10-282-122A-53671

Query Match 83.9%; Score 47; DB 4; Length 279;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 MALPPCHAL 10
DB 157 MALPPCHLL 165

RESULT 32

US-10-282-122A-50921
Sequence 50921, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50921
LENGTH: 323
TYPE: PRT
ORGANISM: Bordetella pertussis
US-10-282-122A-50921

Query Match 83.9%; Score 47; DB 4; Length 323;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 Db 187 MALPPCHLL 195

RESULT 33

US-10-282-122A-67673

; Sequence 67673, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Lianguo

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67673

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-10-282-122A-67673

Query Match 83.9%; Score 47; DB 4; Length 323;

Best Local Similarity 88.9%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 Db 187 MALPPCHLL 195

RESULT 34

US-10-282-122A-69408

; Sequence 69408, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Lianguo

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 69408

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Pseudomonas syringae

US-10-282-122A-69408

Query Match 83.9%; Score 47; DB 4; Length 323;

Best Local Similarity 88.9%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MALPPCHAL 10
 |||||
 Db 187 MALPPCHLL 195

RESULT 35

US-10-958-216-469

; Sequence 469, Application US/10958216

; Publication No. US20050181388A1

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, ALED

; APPLICANT: DHARAMSI, AKIL

; APPLICANT: VEDADI, MASOUD

; APPLICANT: ALAM, MUHAMMAD ZAHOOOR

; APPLICANT: ARROWSMITH, CHERYL

; APPLICANT: AWREY, DONALD E.

; APPLICANT: BEATTIE, BRYAN

; APPLICANT: BUZADZIJIA, KRISTINA

; APPLICANT: CANADIEN, VERONICA

; APPLICANT: DOMAGALA, MEGAN

; APPLICANT: HOUSTON, SIMON

; APPLICANT: KANAGARAJAH, DHUSHY

; APPLICANT: LI, QIN

; APPLICANT: MANSOURY, KAMRAN

; APPLICANT: McDONALD, MERRY-LYNN

; APPLICANT: NETHERY, KATHLEEN

; APPLICANT: NG, IVY


```

; APPLICANT: OUYANG, HUI
; APPLICANT: PINDER, BENJAMIN
; APPLICANT: RICHARDS, DAWN
; APPLICANT: TAI, MATTHEW
; APPLICANT: THALAKADA, ROSANNE
; APPLICANT: VALLEE, FRANCOIS
; APPLICANT: VIRAG, CRISTINA
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
; FILE REFERENCE: IPT-205.01
; CURRENT APPLICATION NUMBER: US/10/958,216
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/CA03/00462
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/369,511
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/385,089
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/385,751
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/386,553
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,577
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,367
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,566
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,390
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/386,601
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1132
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 469
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-958-216-469

```

```

Query Match      82.1%; Score 46; DB 5; Length 55;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 MALPPCHAL 10
      ||||| :
Db      5 MALPPCHTM 13

```

```

RESULT 36
US-10-437-963-163320
; Sequence 163320, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163320
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

```

```

; OTHER INFORMATION: Clone ID: PAT_MRT4530_62327C.1.pgp
US-10-437-963-163320
Query Match      82.1%; Score 46; DB 4; Length 297;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 LMALPPCHA 9
      ||||| :
Db      47 LMALPPCHA 55

```

```

RESULT 37
US-10-282-122A-57222
; Sequence 57222, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57222
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57222

```

```

Query Match      82.1%; Score 46; DB 4; Length 315;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy      2 MALPPCHAL 10
      ||||| :
Db      192 MALPPCHTM 200

```

```

RESULT 38
US-10-958-216-464

```

```

/ Sequence 464, Application US/10958216
/ Publication No. US20050181389A1
/ GENERAL INFORMATION:
/ APPLICANT: EDWARDS, ALED
/ APPLICANT: DHARAMSI, AKIL
/ APPLICANT: VEDADI, MASOUD
/ APPLICANT: ALAM, MUHAMMAD ZAHOOR
/ APPLICANT: ARROWSMITH, CHERYL
/ APPLICANT: AWREY, DONALD E.
/ APPLICANT: BEATTIE, BRYAN E.
/ APPLICANT: BUZADZIJAJ, KRISTINA
/ APPLICANT: CANADINE, VERONICA
/ APPLICANT: DOMAGALA, MEGAN
/ APPLICANT: HOUSTON, SIMON
/ APPLICANT: KANAGARAJAH, DHUSHY
/ APPLICANT: LI, QIN
/ APPLICANT: MANSOURY, KAMRAN
/ APPLICANT: McDONALD, MERRY-LYNN
/ APPLICANT: NETHERY, KATHLEEN
/ APPLICANT: NG, IYV
/ APPLICANT: OUYANG, HUI
/ APPLICANT: PINDER, BENJAMIN
/ APPLICANT: RICHARDS, DAWN
/ APPLICANT: TAI, MATTHEW
/ APPLICANT: THALAKADA, ROSANNE
/ APPLICANT: VALLEE, FRANCOIS
/ APPLICANT: VIRAG, CRISTINA
/ TITLE OF INVENTION: NOVEL PURIFIED P
/ FILE REFERENCE: IPT-205.01
/ CURRENT APPLICATION NUMBER: US/10/95
/ CURRENT FILING DATE: 2004-10-04
/ PRIOR APPLICATION NUMBER: PCT/CA03/0
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/369,511
/ PRIOR FILING DATE: 2002-04-02
/ PRIOR APPLICATION NUMBER: 60/385,089
/ PRIOR FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: 60/385,751
/ PRIOR FILING DATE: 2002-06-04
/ PRIOR APPLICATION NUMBER: 60/386,553
/ PRIOR FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: 60/386,577
/ PRIOR FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: 60/386,367
/ PRIOR FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: 60/386,566
/ PRIOR FILING DATE: 2002-06-05
/ PRIOR APPLICATION NUMBER: 60/386,390
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: 60/386,601
/ PRIOR FILING DATE: 2002-06-06
/ Remaining Prior Application data rem
/ NUMBER OF SEQ ID NOS: 1132
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 464
/ LENGTH: 315
/ TYPE: PR1
/ ORGANISM: Enterococcus faecalis
/ US-10-958-216-464

```

```

Query Match      92.1%; Score 46; DB 5; Length 315;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
         | | | | | | |
Db      192 MALPPCHTM 200

```

RESULT 39
US-10-958-216-466
; Sequence 466, Application US/10958216
; Publication No. US20050181388A1

```

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: ALAM, MUHAMMAD ZAHoor
; APPLICANT: ARROWSMITH, CHERYL
; APPLICANT: AWREY, DONALD E.
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: BUZADZIJIA, KRISTINA
; APPLICANT: CANADIEN, VERONICA
; APPLICANT: DOMAGALA, MEGAN
; APPLICANT: HOUSTON, SIMON
; APPLICANT: KANAGARAJAH, DHUSHY
; APPLICANT: LI, QIN
; APPLICANT: MANSOURY, KAWRAN
; APPLICANT: MCDONALD, MERRY-LYNN
; APPLICANT: NETHERY, KATHLEEN
; APPLICANT: NG, IVY
; APPLICANT: OUYANG, HUI
; APPLICANT: PINDER, BENJAMIN
; APPLICANT: RICHARDS, DAWN
; APPLICANT: TAI, MATTHEW
; APPLICANT: THALAKADA, ROSANNE
; APPLICANT: VALLEE, FRANCOIS
; APPLICANT: VIRAG, CRISTINA
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
; FILE REFERENCE: IPT-205.01
; CURRENT APPLICATION NUMBER: US/10/958,216
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/CA03/00462
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/369,511
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/385,089
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/385,751
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/386,553
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,577
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,367
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,566
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,390
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/386,601
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1132
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 466
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-10-958-216-466

```

Query Match	82.1%	Score 46;	DB 5;	Length 315;
Best Local Similarity	77.8%;	Pred. No. 26;		
Matches	7;	Conservative	1;	Mismatches
				Indels
				0;
				Gaps
				0;
Qy	2	MALPPCHAL	10	
			:	
Db	192	MALPPCHTM	200	

RESULT 40
US-10-282-122A-70335
; Sequence 70335, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu

```

; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70335
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-70335

Query Match      82.1%; Score 46; DB 4; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
Db      196 MALPPCHTM 204
||||||| :

RESULT 41
US-10-282-122A-70576
; Sequence 70576, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```

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; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70576
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70576

Query Match      82.1%; Score 46; DB 4; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
Db      196 MALPPCHTM 204
||||||| :

RESULT 42
US-10-282-122A-70811
; Sequence 70811, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```

```
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70811
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70811

Query Match      82.1%; Score 46; DB 4; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
Db      196 MALPPCHTM 204

RESULT 43
US-10-282-122A-71845
; Sequence 71845, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71845
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (242)..(242)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-71845

Query Match      82.1%; Score 46; DB 4; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
Db      196 MALPPCHTM 204

RESULT 44
US-10-857-625-654
; Sequence 654, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 654
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-857-625-654

Query Match      82.1%; Score 46; DB 5; Length 318;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 MALPPCHAL 10
Db      196 MALPPCHTM 204

RESULT 45
US-09-855-604-277
; Sequence 277, Application US/09855604
; Publication No. US20040214165A1
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: ER 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 277
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; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-277

Query Match      78.6%; Score 44; DB 3; Length 51;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
Db 25 LVSLPPCHPL 34

RESULT 46
US-09-855-604-277
; Sequence 277, Application US/09855604
; Publication No. US20050158714A9
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; PRIOR FILING DATE: 2001-05-16
; PRIOR FILING DATE: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 277
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-277

Query Match      78.6%; Score 44; DB 3; Length 51;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMALPPCHAL 10
Db 25 LVSLPPCHPL 34

RESULT 47
US-09-864-408A-6614
; Sequence 6614, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6614
; LENGTH: 93
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-6614

Query Match      78.6%; Score 44; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8
Db 32 MALPPCH 38

RESULT 48
US-10-425-115-185774
; Sequence 185774, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185774
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .. (135)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_101012C.1.pep
US-10-425-115-185774

Query Match      78.6%; Score 44; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MALPPCH 8
Db 10 MALPPCH 16

RESULT 49
US-09-867-550-396
; Sequence 396, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1 Polynucleotides from Atherogenic Cells and
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 21402-013 (Cura-313)
; CURRENT APPLICATION NUMBER: US/09/867,550
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: USSN 60/208,427
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: wherein Xaa may be any one of Phe or Ser or Tyr or Cys or Leu or
; OTHER INFORMATION: His or Arg or Ile or Thr or Asn or Val or Ala or Asp or Gly
US-09-867-550-396

```

```

Query Match      78.6%; Score 44; DB 3; Length 136;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 MALPPCHAL 10
Db      55 VALPPECHYL 63

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RESULT 50
US-10-767-701-43390
; Sequence 43390, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43390
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C28633_1.pep
US-10-767-701-43390

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```

Query Match      78.6%; Score 44; DB 4; Length 148;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 MALPECH 8
Db      25 MALPECH 31

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Search completed: February 17, 2006, 02:48:20
Job time : 183 secs

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